

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 15:39:34 ; Search time 2651 Seconds
(without alignments)
10727.712 Million cell updates/sec

Title: US-09-786-675-11

Perfect score: 1359
Sequence: 1 atgagaccctcccgagtc.....agttctctcagaagatga 1359

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 30

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

GenBdb:.*
1: gb_da.*
2: gb_hlg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vl.*
30: em_hlg_hum.*
31: em_hlg_inv.*
32: em_hlg_other.*
33: em_hlg_inv.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
------------	-------------	-------	--------	----	-------------

c 1 55 4.0 86743 8 AP003218

AP003218 Oryza sat

ALIGNMENTS

RESULT 1
LOCUS AP003218 86743 bp DNA linear PLN 19-DEC-2001
DEFINITION Oryza sativa genomic DNA, chromosome 1, BAC clone:OSJNB0021A09,
complete sequence.

ACCESSION AP003218
VERSION AP003218.3 GI:17933033

KEYWORDS HTG.
SOURCE Oryza sativa (cultivar:Nipponbare) DNA, clone:OSJNB0021A09.
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 86743)

AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE Direct Submission

JOURNAL Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

COMMENT On Dec 18, 2001 this sequence version replaced gi:17132514.
The orientation of the sequence is from -21M13 to M13rev of the BAC
clone.

FEATURES
source location/qualifiers

1..86743
/organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="1"

BASE COUNT 24257 a 19182 c 18802 g 24502 t
ORIGIN

Query Match 4.0%; Score 55; DB 8; Length 86743;

Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 820 GGATTTCAGAGACGACACTAATTAATTGCTGATGCTTCTACTCCTTTGGCAGG 874

DB 55073 GGATTTCAGAGACGACACTAATTAATTGCTGATGCTTCTACTCCTTTGGCAGG 55019

Search completed: November 1, 2002, 17:08:24
Job time : 2683 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

On nucleic - nucleic search, using sw model

Run on: November 1, 2002, 14:20:34 : Search time 251 Seconds
(without alignments)
9295.963 Million cell updates/sec

Title: US-09-786-675-11

Perfect score: 1359
Sequence: 1 atggacccttccccgcagtc.....agttcttcagaagaatga 1359

Scoring table: OLIGO_MUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 30

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

- N_Ceneseq_032802.*
- 1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
 - 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
 - 3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
 - 4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
 - 5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
 - 6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
 - 7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
 - 8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
 - 9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
 - 10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
 - 11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
 - 12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
 - 13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
 - 14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
 - 15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
 - 16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
 - 17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
 - 18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
 - 19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
 - 20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
 - 21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
 - 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
 - 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
 - 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	ID
1	1359	100.0	1359 21 AA251791
2	62	4.6	1031 21 AA251792

ALIGNMENTS

RESULT 1
AA251791

ID	AA251791 standard; cDNA; 1359 BP.
XX	
AC	AA251791;
XX	
DT	04-JUL-2000 (first entry)
XX	
DE	Corn farnesyltransferase beta subunit cDNA.
XX	
KN	Corn; farnesyltransferase beta subunit; transgenic plant;
XX	drought tolerance; cell growth; ss.
OS	Zea mays.
XX	
FH	Key
FT	Location/Qualifiers
FT	1..1359
FT	/*tag- a
XX	/product- "Farnesyltransferase beta subunit"
PN	W0200014207-A2.
XX	
PD	16-MAR-2000.
XX	
PF	07-SEP-1999; 99MO-US20419.
XX	
PR	08-SEP-1998; 98US-0099521.
XX	
PA	(DUPO) DU PONT DE NEMOURS & CO E. I.
XX	
PI	Cahoon RE, Miao G, Powell W;
XX	
DR	WPI: 2000-256964/22.
DR	P-PSDB: AAY70502.
PT	New isolated polynucleotide encoding farnesyltransferase polypeptide is
PT	useful for producing transgenic plants with an altered level of
XX	farnesyltransferase -
PS	Claim 3; Page 38-39; 51pp: English.
XX	
CC	The present sequence is a cDNA encoding farnesyltransferase beta subunit
CC	from clone p0127.cntbu.1br isolated from corn nucellus tissue
CC	cDNA library. The present sequence is used in the construction
CC	of a chimeric gene to produce transgenic plants with altered level
CC	of farnesyltransferase subunit. Plants with decreased farnesyltransferase
CC	activity may have enhanced tolerance to drought stress. Nucleic acids
CC	encoding all or a part of farnesyltransferase proteins can be used in
CC	studies to understand cell growth in plants and provide genetic tools to
CC	control cell growth and improve tolerance to drought in mature plants.
XX	
SQ	Sequence 1359 BP: 340 A: 308 C: 351 G: 360 T: 0 other:
Query Match	100.0%; Score 1359; DB 21; Length 1359;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1359;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGGACCCCTCCCGCAGTGCAGCCGCCACCGAGACGCCGCGCGCGGAT 60
DB	1 ATGGACCCCTCCCGCAGTGCAGCCGCCACCGAGACGCCGCGCGCGGAT 60
QY	61 CCCGACCTACGAGGCTCAGCGTGACGACGAGTGCAGATGAAGTGGAGCCAGGGTT 120
DB	61 CCCGACCTACGAGGCTCAGCGTGACGACGAGTGCAGATGAAGTGGAGCCAGGGTT 120
QY	121 GCGGACATCTACGCGCTCCCTCTTCGGGGCGCGGCCACACGAAATCCATCATCTAGTAG 180
DB	121 GCGGACATCTACGCGCTCCCTCTTCGGGGCGCGGCCACACGAAATCCATCATCTAGTAG 180
QY	181 CTGTGCGGTATCAGCATATTCAGATATTCAGCCCTGGGCTGAGCATATGGACACACC 240
DB	181 CTGTGCGGTATCAGCATATTCAGATATTCAGCCCTGGGCTGAGCATATGGACACACC 240
QY	241 TTTCATGTTTCTAGATGCCAATCGCCCTGGCTATGCTACTGATGATGCTTATCCACTGCT 300
DB	241 TTTCATGTTTCTAGATGCCAATCGCCCTGGCTATGCTACTGATGATGCTTATCCACTGCT 300

```

Db 241 TTTTCATGTTCTAGATGCCAATCGCCCTTGGCTATGCTACTGATGGTTCATCGACTTGGT 300
Oy 301 TTGCGTGATGAAGCACTTGATGATGATCTTGAGATGATATCATACACTTCTTAACTGCA 360
Db 301 TTTGCTGATGAAGCACTTGATGATGATCTTGAGATGATATCATACACTTCTTAACTGCA 360
Oy 361 TGTCAAGATAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 TGTCAAGATAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Oy 421 ACTTATGCTGCTAAATACACTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db 421 ACTTATGCTGCTAAATACACTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Oy 481 AATAGGGCAACCTGTACAAATTTATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 AATAGGGCAACCTGTACAAATTTATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 540
Oy 541 ATGCAATGATGCTGCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 541 ATGCAATGATGCTGCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Oy 601 CTTGTGAATATCTTGTGATTTTAACTGGCAAAAGTGTAGGCGACTACATACAGATGATGAT 660
Db 601 CTTGTGAATATCTTGTGATTTTAACTGGCAAAAGTGTAGGCGACTACATACAGATGATGAT 660
Oy 661 CAACCTTATGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 661 CAACCTTATGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Oy 721 TTTCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 TTTCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Oy 781 TTTGATTTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 840
Db 781 TTTGATTTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 840
Oy 841 AAATTTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 841 AAATTTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Oy 901 TTTATTTAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 901 TTTATTTAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Oy 961 GAGGATGCTGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1020
Db 961 GAGGATGCTGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1020
Oy 1021 GACTATGCGAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1021 GACTATGCGAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Oy 1081 CATTAACATTTGCTGCAACAATACATCTTCTGAGTACTAGAGGAGGCTTG 1140
Db 1081 CATTAACATTTGCTGCAACAATACATCTTCTGAGTACTAGAGGAGGCTTG 1140
Oy 1141 AGGAGTAAAGCTGCAACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
Db 1141 AGGAGTAAAGCTGCAACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
Oy 1201 GCAGTTAGCCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 1260
Db 1201 GCAGTTAGCCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 1260
Oy 1261 CTTGACCGCTACTGTAATTTGCTGAGAGCAATGATGATGATGATGATGATGATGATGATGAT 1320
Db 1261 CTTGACCGCTACTGTAATTTGCTGAGAGCAATGATGATGATGATGATGATGATGATGATGAT 1320
Oy 1321 AAGTACATACAGCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1359
Db 1321 AAGTACATACAGCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1359

```

```

RESULT 2
AA251792
ID AA251792 standard; cDNA; 1031 BP.
XX
AC AA251792;
XX
DE Rice farnesyltransferase beta subunit cDNA.
XX
KW Rice: farnesyltransferase beta subunit; transgenic plant;
XX drought tolerance; cell growth; ss.
XX
OS Oryza sativa.
XX
FH Key location/Qualifiers
FT CDS 91..1029
FT /*tag= a
FT /product= "Farnesyltransferase beta subunit"
FT /note= "Does not include stop codon"
FT /partial
PN MO200014207-A2.
XX
PD 16-MAR-2000.
XX
PE 07-SEP-1999; 99MO-US20419.
XX
PR 08-SEP-1998; 98US-0099521.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E. I.
XX
PI Cahoon RE, Miao G, Powell W;
XX
DR WPI: 2000-256964/22.
XX
DR P-PSDB: MAY70503.
XX
PT New isolated polynucleotide encoding farnesyltransferase polypeptide is
PT useful for producing transgenic plants with an altered level of
PT farnesyltransferase.
XX
PS Claim 3; Page 40-41; 51pp; English.
XX
CC The present sequence is a cDNA encoding farnesyltransferase beta subunit
CC from clone rlr24.pk0007.de isolated from rice infected leaf
CC cDNA library rlr24. The present sequence is used in the construction
CC of a chimeric gene to produce transgenic plants with altered level
CC of farnesyltransferase subunit. Plants with decreased farnesyltransferase
CC activity may have enhanced tolerance to drought stress. Nucleic acids
CC encoding all or a part of farnesyltransferase proteins can be used in
CC studies to understand cell growth in plants and provide genetic tools to
CC control cell growth and improve tolerance to drought in mature plants.
XX
SQ Sequence 1031 BP; 228 A; 249 C; 302 G; 252 T; 0 other;

```

```

Query Match 4.6%; Score 62; DB 21; Length 1031;
Best Local Similarity 100.0%; Pred. No. 8.4e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 820 GGATTTCAAGACGACAACTAATTAATTTGTTGATGTTGCTACTCTTTTGGCAGGAGCT 879
Db 928 GGATTTCAAGACGACAACTAATTAATTTGTTGATGTTGCTACTCTTTTGGCAGGAGCT 987
Oy 880 GC 881
Db 988 GC 989

```

Search completed: November 1, 2002, 15:53:15
Job time : 252 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 15:40:44 ; Search time 56 Seconds
(without alignments)
5960.999 Million cell updates/sec

Title: US-09-786-675-11

Perfect score: 1359
Sequence: 1 atggaccctcccgagtc.....agttcttcagaagatga 1359

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 12816752 residues

Word size : 30

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

- 1: Issued_Patents_NA:*
- 2: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
No matches found					

Search completed: November 1, 2002, 17:09:02
Job time : 56 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 14:50:49 ; Search time 1797 Seconds

(without alignments)
10207.213 Million cell updates/sec

Title: us-09-786-675-11

Perfect score: 1359

Sequence: 1 atgaccctcccccgcagtc.....agctctctcagaagagtga 1359

Scoring table: OLIGO_MTC

Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 674847542 residues

Word size : 30

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:*
1: em_estba:*
2: em_estbun:*
3: em_estlin:*
4: em_estlun:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estc:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_jov:*
15: em_gss_pln:*
16: em_gss_vtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	242	17.8	521	9	BE129712 946003D09
2	232	17.1	533	9	AM120078 614083B05
3	82	6.0	417	9	AM146746 614083B05
4	66	4.9	191	12	AZ916116 PstI 2, h6
5	32	2.4	582	9	BE194182 HVSMB008
6	32	2.4	675	9	AL506683 AL506683
7	32	2.4	715	9	BE214204 HIV_CEB000

ALIGNMENTS

RESULT 1
BE129712/c
LOCUS
DEFINITION
521 bp mRNA linear EST 21-JUN-2000
946003D09.X1 946 - tassal primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.

ACCESSION BE129712
VERSION BE129712.1 GI:8577075
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
AUTHORS 1 (bases 1 to 521)
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946003 row: D column: 09.
FEATURES
source
location/Qualifiers
1..521
/organism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tassal primordium prepared by Schmidt lab"
/tissue_type="tassels"
/dex_stage="just after the transition from vegetative to inflorescence development"
/lab_host="X10LR"
/note="Organ: tassels; Vector: HybridZAP; Site:1: EcorI; Site:2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridZAP. Sample insert size range was 350 bp to 3 kb with a 1 kb average."

BASE COUNT
151 a 118 c 97 g 155 t
ORIGIN

Query Match 17.8%; Score 242; DB 9; Length 521;

Best local Similarity 100.0%; Pred. No. 1.2e-115;

Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1118	CTCAGTACTAGAGGAGCTTGAGGATAGCCTGGAAGACAGATCACTATCATT	1177
DB	371	CTCAGTACTAGAGGAGCTTGAGGATAGCCTGGAAGACAGATCACTATCATT	312
QY	1178	CATGCTACTGCTCAGTGCCCTGCAGTTAGCCAGTACAGTGCATGATGATGTT	1237
DB	311	CATGCTACTGCTCAGTGCCCTGCAGTTAGCCAGTACAGTGCATGATGATGTT	252
QY	1238	CGTGCCATTACTACAGATGCTTGACCGTACTATTTGCTGCGACCAATCCATC	1297
DB	251	CGTGCCATTACTACAGATGCTTGACCGTACTATTTGCTGCGACCAATCCATC	192
QY	1298	CACCTACAACTGCTCCTAGATAGTACATCAGCCTATGATGCTTCTCAGAAGAGT	1357
DB	191	CACCTACAACTGCTCCTAGATAGTACATCAGCCTATGATGCTTCTCAGAAGAGT	132
QY	1358	GA 1359	
DB	131	GA 130	

RESULT 2
AM120078
LOCUS
DEFINITION
ACCESSION
VERSION
533 bp mRNA linear EST 22-OCT-1999
614083B05.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA,
AM120078 mRNA sequence.
AM120078.1 GI:6095411
KEYWORDS EST.

SOURCE Zea mays.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 533)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614083 row: B column: 05.
Location/Qualifiers
1. 533
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_id="614 - root cDNA library from Walbot Lab"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XL0LR"
/note="Organ: root; Vector: pBluescriptII SK+; Site_1: EcoRI; Site_2: XhoI; 3-4 days old root tissue from Walbot Lab (LM)"

BASE COUNT 157 a 109 c 103 g 162 t 2 others
ORIGIN

Query Match 17.1%; Score 232; DB 9; Length 533;
Best Local Similarity 100.0%; Pred. No. 2.1e-110;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1118 CTCAGTACTAGAGGAGCGTTGAGGATAGCCTGGAAGACAGATCACTATCAT 1177
|||||
DB 302 CTCAGTACTAGAGGAGCGTTGAGGATAGCCTGGAAGACAGATCACTATCAT 361
|||||
QY 1178 CATGCTACTGCGCTCAGTGGCGCTGAGCTAGGACAGTACAGTGCATGACTGATGCTT 1237
|||||
DB 362 CATGCTACTGCGCTCAGTGGCGCTGAGCTAGGACAGTACAGTGCATGACTGATGCTT 421
|||||
QY 1238 CCGGCCATTACTCAGCATGCTGAGCGTACTCTATTGTCGGAGCCCAATCCATC 1297
|||||
DB 422 CCGGCCATTACTCAGCATGCTGAGCGTACTCTATTGTCGGAGCCCAATCCATC 481
|||||
QY 1298 CACTCTACAAATGTTCTCTAGATAGACATACAGCCATAGATTCTTCTC 1349
|||||
DB 482 CACTCTACAAATGTTCTCTAGATAGACATACAGCCATAGATTCTTCTC 533
|||||

RESULT 3
LOCUS AM146746 417 bp mRNA linear EST 03-NOV-1999
DEFINITION 614083B05.y2 614 - root cDNA library from Walbot Lab Zea mays cDNA,
mRNA sequence.
ACCESSION AM146746
VERSION AM146746.1 GI:6194642
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 417)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V

Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614083 row: B column: 05.
Location/Qualifiers
1. 417
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_id="614 - root cDNA library from Walbot Lab"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XL0LR"
/note="Organ: root; Vector: pBluescriptII SK+; Site_1: EcoRI; Site_2: XhoI; 3-4 days old root tissue from Walbot Lab (LM)"

BASE COUNT 131 a 79 c 79 g 128 t
ORIGIN

Query Match 6.0%; Score 82; DB 9; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.2e-31;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1118 CTCAGTACTAGAGGAGCGTTGAGGATAGCCTGGAAGACAGATCACTATCAT 1177
|||||
DB 336 CTCAGTACTAGAGGAGCGTTGAGGATAGCCTGGAAGACAGATCACTATCAT 395
|||||
QY 1178 CATGCTACTGCGCTCAGTGGCGCT 1199
|||||
DB 396 CATGCTACTGCGCTCAGTGGCGCT 417
|||||

RESULT 4
LOCUS A2916116/c 191 bp DNA linear GSS 15-MAR-2001
DEFINITION Psst1.2.h6-c-1.0 Maize Psst B73 Leaf Zea mays genomic, DNA sequence.
ACCESSION A2916116
VERSION A2916116.1 GI:1347388
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 191)
AUTHORS Missouri Maize Project--Maize Mapping Project.
TITLE Psst1 Zea mays B73 Psst leaf tissue library
JOURNAL Unpublished (2001)
COMMENT Contact: Schroeder S
Missouri Maize Project--Maize Mapping Project
University of Missouri
209 Curtis Hall, Columbia, MO 65211, USA
Tel: 573 882 8214
Fax: 573 884 7850
Email: aschroeder@celephais.agron.missouri.edu
Class: shotgun.

FEATURES
source Location/Qualifiers
1. 191
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_id="Maize Psst B73 Leaf"
/tissue_type="Leaf"
/lab_host="DH5 alpha"
/note="Organ: Leaf; Vector: PUC19; Psst digested B73 genomic sucrose gradient size fractionated fragment sizes of 0.5kb to 2kb ligated to PUC19 transformed in DH5 alpha"

BASE COUNT 81 a 36 c 27 g 47 t
ORIGIN

Query Match 4.9%; Score 66; DB 12; Length 191;
 Best Local Similarity 100.0%; Pred. No. 2.4e-23;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 591 GGTGGCAGGCTGTGATATCTTATTTAACTGCGAAAGGTAGCGACTACAT 650
 |||||||
 Db 162 GGTGGCAGGCTGTGATATCTTATTTAACTGCGAAAGGTAGCGACTACAT 103

QY 651 AGCAAG 656
 ||||||
 Db 102 AGCAAG 97

RESULT 5
 BE194182
 LOCUS
 DEFINITION HVSMEH0084H13f Hordeum vulgare 5-45 DAP spike EST library
 HYCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH0084H13f,
 mRNA sequence.

ACCESSION BE194182 582 bp mRNA linear EST 22-OCT-2001
 VERSION BE194182.1 GI:8706368
 KEYWORDS EST.
 SOURCE Hordeum vulgare
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.
 1 (bases 1 to 582)
 Wing,R., Close,T.J., Kleinof,A., Wise,R., Begum,D., Frisch,D., Yu
 ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
 ,R.D., Close,S.J., Gates,R. and Main,D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex 5-45 DAP spike cDNA library
 Unpublished (2001)
 Contact: Wing RA
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: twing@clemson.edu
 Total hg bases = 161
 Seq primer: AATTACCTCCTCAGTAAAGC
 High quality sequence start: 12
 High quality sequence stop: 527.
 Location/Qualifiers
 1..582
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone_lib="HVSMEH0084H13f"
 /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
 HYCDNA0009 (5 to 45 DAP)"
 /tissue_type="5-45 DAP Spike"
 /lab_host="SOLR"
 /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
 plants were grown in the greenhouse at the University of
 California, Riverside (Fenton, SJ Close, TJ Close, Fenton
 spikes with awns trimmed were collected at 5, 10, 15, 20,
 30 and 45 DAP (Fenton). Total RNA was prepared from each
 pool, equal quantities of all six RNA pools were combined,
 poly(A) RNA was purified from the mixture, one primary
 unamplified cDNA library was made, and 1 million pfu were
 in vivo excised to give plasmid SK(-) cDNA phagemids
 (Choi) in the TJ Close lab at the University of California,
 Riverside. Phagemids were plated and picked at the Clemson
 University Genomics Institute (CUGI) (Begum, Palmer,
 Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
 sequencing and sequence analysis were performed at CUGI
 (Wing, Yu, Frisch, Henry, Simmons, Gates, Rambo, Main).
 The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and

sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
 this clone see <http://www.genome.clemson.edu/orders> Also
 see Close TJ, Wing R, Kleinof A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)

BASE COUNT 123 a 168 c 176 g 114 t 1 others

ORIGIN

Query Match 2.4%; Score 32; DB 9; Length 582;
 Best Local Similarity 100.0%; Pred. No. 2.4e-05;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 GTGACGCGAGTGAGCAGATGAGGTGAGGC 113
 |||||||
 Db 171 GTGACGCGAGTGAGCAGATGAGGTGAGGC 202

RESULT 6
 AL506683
 LOCUS
 DEFINITION AL506683 Hordeum vulgare Barke developing caryopsis (3..15.DAP)
 Hordeum vulgare cDNA clone HY03022F 5', mRNA sequence.

ACCESSION AL506683 675 bp mRNA linear EST 04-JAN-2001
 VERSION AL506683.1 GI:12032898
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.
 1 (bases 1 to 675)
 Michalek,W., Wessche,W., Pleissner,K.-P. and Graner,A.
 EST sequencing and analysis in barley
 Unpublished (2000)
 Contact: Michalek W
 Institute for Plant Genetics and Crop Plant Research
 Corrensstr.3, D-06466 Gatersleben, Germany
 Email: michalek@ipk-gatersleben.de, <http://iprc.ipk-gatersleben.de>
 Seq primer: T3 primer for 5'end.
 Location/Qualifiers
 1..675
 /organism="Hordeum vulgare"
 /cultivar="Barke"
 /db_xref="taxon:4513"
 /clone_lib="HY03022F"
 /clone_lib="Hordeum vulgare Barke developing caryopsis
 (3..15.DAP)"
 /tissue_type="developing caryopsis (3..15.DAP)"
 /lab_host="XOGR"
 /note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2:
 XhoI; mRNA was made from developing caryopsis (3..15.DAP)
 of spring barley variety 'Barke', a high quality malting
 variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI
 (3'-end of cDNA). NOTE: Due to a cloning artefact caused
 by the kit, in most cases the EcoRI site is NOT present,
 as well as the EcoRI adapter. Average insert size is 1 kb
 Sequence trimming: Vector sequences and sequence ends were
 trimmed from the 5'-and 3'-end until a 50 bp window
 contains less than two ambiguities. The maximum length was
 set to 700 bp"

BASE COUNT 149 a 185 c 199 g 138 t 4 others

ORIGIN

Query Match 2.4%; Score 32; DB 9; Length 675;
 Best Local Similarity 100.0%; Pred. No. 2.5e-05;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 GTGACGCGAGTGAGCAGATGAGGTGAGGC 113
 |||||||
 Db 191 GTGACGCGAGTGAGCAGATGAGGTGAGGC 222

RESULT 7
 BE214204 715 bp mRNA linear EST 23-Oct-2001
 LOCUS HV_CEB0002K12f Hordeum vulgare seedling green leaf EST library
 DEFINITION HV_CEB0002K12f, Blumeria challenged) Hordeum vulgare cDNA clone
 BE214204
 VERSION BE214204.3 GI:16335375
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 715)
 Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D.,
 Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi
 D.W., Fenton, R.D., Oates, R. and Maito, D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Blumeria infected incompatible (Mla6) seedling
 leaf cDNA library
 Unpublished (2001)
 On Jul 3, 2000 this sequence version replaced gi:13263971.
 JOURNAL Contact: Wing RA
 COMMENT Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hg bases = 422
 Seq primer: AATTACCTCTACTAAAGCG
 High quality sequence stop: 555.
 Location/Qualifiers
 1..715
 /organism="Hordeum vulgare"
 /cultivar="C116151 (Mla6)"
 /db_xref="taxon:4513"
 /clone="HV_CEB0002K12f"
 /clone_lib="Hordeum vulgare seedling green leaf EST
 library (VCDNA0005 (Blumeria challenged))"
 /library (VCDNA0005 (Blumeria challenged))"
 /issue_type="seedling green leaf"
 /lab_host="SOLR"
 /note="Vector: lambdaZAP. Site_1: EcoRI; Site_2: XhoI;
 C.I. 16151 (Mla6) plants were greenhouse grown in the R
 wise lab at Iowa State University, Ames, IA; 7 day old
 green seedlings were challenged with isolate 5874 (AVRMLa6
) of Blumeria graminis f. sp. hordei, and leaves were
 harvested 20 and 24 hr post-inoculation and snap frozen;
 uninoculated leaves were harvested 20 hr post-inoculation
 (Wei, Wise). In the T3 Close lab at the University of
 California, Riverside, total RNA was prepared from each
 sample pool, equal quantities of all three RNA pools were
 combined, poly(A) RNA was purified from the mixture, one
 primary unamplified cDNA library was made, and 1 million
 pfu were in vivo excised to give Bluescript SK(-) cDNA
 phagemids (Choi, Close). Phagemids were plated and picked
 at the Clemson University Genomics Institute (CUGI) (Begum
 , Palmer, Frisch, Atkins and Wing). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
 , Rambo, Maito). The sequence has been trimmed to remove
 vector sequence and contains a minimum of 100 bases of
 phred value 20 or above. For more details on library
 preparation and sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders
 see Close T.J., Wing R., Kleinhofs A., Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/ggpages/bjn/31/cover.html)"
 189 c 219 g 145 t

ORIGIN

Query Match 2.48; Score 32; DB 9; Length 715;
 Best Local Similarity 100.0%; Pred. No. 2.6e-05;
 Matches 32; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 Oy 82 GTGACGACGTGAGACAGATGAAGTGAAGCC 113
 ||||||||||||||||||||||||||||||||
 Db 172 GTGACGACGTGAGACAGATGAAGTGAAGCC 203

Search completed: November 1, 2002, 16:23:28
 Job time : 1799 secs

BASE COUNT

162 a 189 c 219 g 145 t

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2002, 12:41:24 ; Search time 2651 Seconds
(without alignments)
10727.712 Million cell updates/sec

Title: US-09-786-675-11

Perfect score: 1359
Sequence: 1 atgagccctcccccgcagtc.....agttcttcacagaagatga 1359

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_or:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_hlg_hum:*
31: em_hlg_in:*
32: em_hlg_other:*
33: em_higo_in:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
------------	-------------	--------	-------	-------------

1	452.2	33.3	1449	8	NGU73203	U73203 Nicotiana	9	U83708 Lycopersico
2	452.2	33.3	1832	8	LEUB83708	L88664 Pea farinose		
3	449.4	33.1	1648	8	PEARFARNES	AF214106		
4	424.8	31.3	1627	8	AF214106	U44849 Arabidopsis		
5	402	29.6	1331	8	ATU44849	AR072721 Sequence		
6	206.6	15.2	2464	6	AR077271	AR102373 Sequence		
7	206.6	15.2	2464	6	AR102373	112220 Sequence 4		
8	206.6	15.2	2464	6	112220	M69056 Rat farinose		
9	206.6	15.0	1413	6	AR102375	AR102375 Sequence		
10	203.6	14.9	1314	6	AR048524	AR048524 Sequence		
11	202	14.9	1314	6	AR048524	AR048524 Sequence		
12	202	14.9	1314	6	AR048524	AR048524 Sequence		
13	202	14.9	1314	6	AR048524	AR048524 Sequence		
14	200.4	14.7	1248	6	AR077273	AR077273 Sequence		
15	200.4	14.7	1248	6	112222	112222 Sequence 8		
16	200.4	14.7	1248	6	HUMPTB	L10414 Human farne		
17	199.2	14.7	1314	6	AR048522	AR048522 Sequence		
18	199.2	14.7	1314	6	BOVPTB	L00633 Bovine farne		
19	187.2	14.5	2546	6	AR048533	AR048533 Sequence		
20	179.6	13.2	86743	8	AP003218	AP003218 Oryza sat		
21	153.6	11.8	40961	3	CBRG27B19	AC084541 Caenorhab		
22	153.6	11.3	1588	3	AY051869	AY051869 Drosophila		
23	144	10.6	34882	3	AC014444	AC014444 Drosophila		
24	144	10.6	199653	3	AC011615	AC011615 Drosophila		
25	144	10.6	225755	3	AE003713	AE003713 Drosophila		
26	112.2	8.3	27797	3	CEP33812	277659 Caenorhabdl		
27	110	8.1	63923	2	AC008292	AC008292 Drosophila		
28	87.4	6.4	43880	8	SPAC17G6	299163 S.pombe chr		
29	83.4	6.1	1958	8	YSCDPR	M22753 S.cerevisia		
30	83.4	6.1	2060	8	SCYDL050C	Z74138 S.cerevisia		
31	83.4	6.1	38516	8	SCCHRIVLA	X95644 S.cerevisia		
32	81	6.0	13066	8	U75644	U75644 Lycopersico		
33	78.2	5.8	3174	8	ATU46574	U46574 Arabidopsis		
34	78.2	5.8	61001	8	AB010699	AB010699 Arabidopsis		
35	59.2	4.4	1758	3	AF230369	AF230369 trypanoso		
36	59	4.3	1306	6	AR123105	AR123105 Sequence		
37	59	4.3	1306	6	AR177716	AR177716 Sequence		
38	56	4.1	1138	6	HSU49245	U93245 Human geran		
39	54.6	4.0	15449	2	AC096084	AC096084 Rattus no		
40	54.4	4.0	1179	9	HSGG11	X98001 H.sapiens m		
41	54.4	4.0	1526	9	BC020790	BC020790 Homo sapi		
42	52.8	3.9	1374	9	HSRABGTRB	Y08201 Homo sapien		
43	51.6	3.8	69622	2	AC101674	AC101674 Mus muscu		
44	51.4	3.8	190517	9	CNS010X4	AL139022 Human chr		
45	49.2	3.6	1230	6	AR123106	AR123106 Sequence		

ALIGNMENTS

RESULT 1	NGU73203	1449 bp	mRNA	linear	PLN 17-DEC-1996
LOCUS	NGU73203				
DEFINITION	Nicotiana glutinosa farinose beta subunit mRNA, partial				
VERSION	U73203				
KEYWORDS	U73203.1 GI:1732586				
SOURCE					
ORGANISM	Nicotiana glutinosa.				
	Nicotiana glutinosa				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
	Asteridae; eustersids I; Solanales; Solanaceae; Nicotiana.				
REFERENCE	1 (bases 1 to 1449)				
AUTHORS	Zhou,D., Yang,Z., and Cramer,C.L.				
TITLE	A cDNA Clone Encoding the beta Subunit of Protein				
	Farinoseyltransferase from Nicotiana glutinosa (Accession No.				
	U73203)(PGR96-109)				
JOURNAL	Plant Physiol. 112, 1398 (1996)				
REFERENCE	2 (bases 1 to 1449)				
AUTHORS	Zhou,D., Yang,Z., and Cramer,C.L.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-OCT-1996) Plant Pathology, Physiology and Weed				

Science, Virginia Polytechnic Institute and State University, 317
Fralin Biotech Center, Blacksburg, VA 24061, USA

FEATURES

source
1..1449
/organism="Nicotiana glauca"
/db_xref="taxon:35889"
CDS
1..1341
/EC_number="2.5.1.21"
/note="Frase"
/product="farnesyltransferase beta subunit"
/protein_id="AB38796.1"
/db_xref="GI:1732587"
/translation="GTSGTTLDEDMVVEREYFYSIPNSHLETSTEHEDY
LTKRLKLPSEFVLDANRPLCWLILHSIALIGESIDAELENDALIDFLSRCODEDGG
YGGPGMPHLATYAAVNSLITLSPKLSINREKLYTFMLQMDTSGFPMHGG
EYRACVTAISVASILOVDELINDVGNVILSCOTTEGIAEPSEAHGYTCG
LAAMILINRANRDLRLIDVFRVGGGGGPGTNNLVGGCSPMAAVATLQRL
KSTVEDIGLSNELSTESADSESELSDPEHLGTSNHYKCTPLDCEQENASPT
KIADTCDFPNRTIARPYRDFEYLQOYVLLCSQIDGFRDKPKGDHHTCYCLSG
LSTAOISWTRERADPLPNDVPGYSQNLRLQHLINVLNDRYFARSFSCV"

BASE COUNT 410 a 274 c 341 g 422 t
ORIGIN

Query Match 33.3% Score 452.2; DB 8; Length 1449;
Best Local Similarity 62.0%; Pred. No. 6.2e-109;
Matches 837; Conservative 0; Mismatches 440; Indels 72; Gaps 5;

71 CGAGCTCAGCTGACGACGAGTGGAGATGAGTGGAGCGCCAGGCTGGCGCATCT 130
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
5 CGAGGGGACGACGACGACGATGAGTGGAGTGGAGCGCGTGGAGATAT 64
131 ACCGCTCCCTCTGGGGGCGCGCCACAGAAATCCATCATCTAGAGCTGTGGCTG 190
111 111 111 111 111 111 111 111 111 111 111 111 111 111
65 ACAATTTTCTACAGCATTCGCCCAATTCGCACT-----TAGAGACTTCAGAG 115
191 ATCAGCATATGAGTATCTGACGCGCTGGGTGAGCATATGGACAGGCTTTTCAATG 250
111 111 111 111 111 111 111 111 111 111 111 111 111 111
116 AAAACGACTTGCATTAATCTCAGTGGAGAAACCTTGCCTGCTCCGCT 175
251 TTAGATGCCAATCGCCCTTGGCTATGCTAGTGGTTCATCCACTTGGCTTGTGATG 310
111 111 111 111 111 111 111 111 111 111 111 111 111 111
176 TCGATGCTAAATGACACATGCTTGTACGTGATCATTCATCATCGCTTTGGGAG 235
311 AAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 370
111 111 111 111 111 111 111 111 111 111 111 111 111 111
236 AATCTATTGATGACCAATGAGAAATGATGATGATGATGATGATGATGATGATG 295
371 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 430
111 111 111 111 111 111 111 111 111 111 111 111 111 111
296 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 355
431 CTGTAATACACTTGTGCAATAGGAGCAAGAGCATTTGATCAATCAATAGGCGCA 490
111 111 111 111 111 111 111 111 111 111 111 111 111 111
356 CAGTCAATTCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 415
491 ACCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 550
111 111 111 111 111 111 111 111 111 111 111 111 111 111
416 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 475
551 GTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 610
111 111 111 111 111 111 111 111 111 111 111 111 111 111
476 GTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 535
611 ACCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 670
111 111 111 111 111 111 111 111 111 111 111 111 111 111
536 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 595
671 AAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 730
111 111 111 111 111 111 111 111 111 111 111 111 111 111
596 AAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655
731 TGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 790

656 TGGCGCAATATCTCTGATTAACCAAGCAATGATGATGATGATGATGATGATGATGAT 715
111 111 111 111 111 111 111 111 111 111 111 111 111 111
791 GGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 850
111 111 111 111 111 111 111 111 111 111 111 111 111 111
716 GGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 775
851 ATGGTGTACTCTCTTTGGCAGGAGCTCCATTCCTTCACACAAAGTAAATATGCA 910
111 111 111 111 111 111 111 111 111 111 111 111 111 111
776 ATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 835
911 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 966
836 CAGTCAATGAAACCTAGGGCTGCAAAATGACATGATGATGATGATGATGATGATGAT 895
967 -----GCTCGACACAGTGTATATG 989
896 CGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955
990 GTGACGCC-----GAAAAGCTTCTCTGCTGTGACATGATGATGATGATGATGAT 1033
956 CTGGCCCTTTGGACAAAGAGACAGAAATGCTTCAGATGCCACAAAGATAGCAGATA 1015
1034 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1093
1016 CTGGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1075
1094 TGCACCAATATATCTCTCTTGTCTGAGTACTAGAGGAGCTTGGAGGATAGCTG 1153
1076 TGCACCAATATATCTCTCTCTGCTCCAG--ATAGATGAGAGTGTGAGACAAACCTG 1132
1154 GAAAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1213
1133 GGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1192
1214 AAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1273
1193 ATAGCTGACCAACAGAGAGTATGATGATGATGATGATGATGATGATGATGATGAT 1252
1274 CT---ATTGCTGAGACCAATCCATCCATGATGATGATGATGATGATGATGATGATGAT 1310
1253 CTCAAAATCTTTGGAACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1312
1331 CAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1359
1313 AAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1341

RESULT 2
LEU83708 1832 bp mRNA linear PLN 25-MAR-1997
LOCUS
DEFINITION Lycopersicon esculentum farnesyl protein transferase subunit B
(LEF7) mRNA, complete cds.
ACCESSION U85708
VERSION U85708.1 GI:1815667
KEYWORDS
SOURCE
ORGANISM
tomato.
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; Eusterales I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE
1 (bases 1 to 1832)
Yakovlevy, S., Trueblood, C.E., Callan, K.L., Narita, J.O.,
Jenkins, S.M., Rine, J. and Grusissem, W.
Plant farnesyltransferase can restore yeast Ras signaling and
mating
Mol. Cell. Biol. 17 (4), 1986-1994 (1997)
MEDLINE
97219988
REFERENCE
2 (bases 1 to 1832)
Yakovlevy, S., Callan, K.L., Narita, J.O. and Grusissem, W.
Direct Submission
TITLE
JOURNAL
Submitted (03-JAN-1997) Plant and Microbial Biology, University of

/db_xref="taxon:3888"
/issue-type="epical bud"
/dev_stage="seedling"
/issue_lib="Clontech"
85.1344
/note="The predicted amino acid sequence shows 48% and 40% identity to the rat and yeast counterparts, respectively:
putative"
/codon_start=1
/product="farnesyl-protein transferase beta-subunit"
/protein_id="AA33649.1"
/db_xref="GI:169049"
/translation="MEASTAEPTPTVSQSDQWIVESQVEHLYOLEFANIPNQSII
RPLCYWIIHISALGESIDDDLENTVFLRCDPNCVAGVGQPHLATTAAV
NLTLLGKESLASINRNKLYGFRMRKPNPGRHDEIDVACYATSAVSIVN
ILDELKINVDLISQTYEGGLAGEPSGAEHGTGGLAAMLLIEGVARLDPL
LDVAVPRQKRGCGFRGTRKLVDCYSEFQAGAVALLORHISIDDEOMAPSEPTVS
DAPEKSLDCTSHATSRHRCMNESSSVYKNTGYNFISERQSPLEPHSLALQ
YILCSODQDQGLRDKRKRDRHNSCTGLSLDQYISMRPDSPLPVMGPYS
NLEPIHPLFRNVLDKREHFEFSOL"
1648
polya_site
BASE COUNT 461 a 316 c 377 g 494 t
ORIGIN
Query Match 33.1% Score 449.4; DB 8; Length 1648;
Best local similarity 63.7% Pred. No. 3,5e-108;
Matches 731; Conservative 0; Mismatches 386; Indels 30; Gaps 2;
QY 243 TCATGTTCTAGATGCCATGCGCCCTGGCTATGCTACTGATGCTGATGCTGCTT 302
DB 198 TAACGCCCATATCATTCGACCTGGCTGTCTGTTACTGATTAATTCATTCATTCCTT 257
QY 303 GCTGATGAAGCACTTGATGATGATCTTGAGAAATATATATGATGATGATGATGAT 362
DB 258 GTTGGGCAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 317
QY 363 TCAGGATAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 422
DB 318 CCGAGATCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 377
QY 423 TTATGCTGCTTAATATACACTTGTGACATAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 482
DB 378 TTATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 437
QY 483 TAGGGGCAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 542
DB 438 TAGAAATTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 497
QY 543 GCATGATGCTGCGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 602
DB 498 GCATGATGCGGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 557
QY 603 TGTGATATTTCTGATTTTAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 662
DB 558 TGTGATCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 617
QY 663 AACTATGAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 722
DB 618 AACTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 677
QY 723 CTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 782
DB 678 TTGTGAGTTAGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 737
QY 783 GATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 842
DB 738 ACTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 797
QY 843 ATTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
DB 798 ATTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 857
QY 903 AATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 945

DB 858 ACATTTCTATTTATGCGAACAATGCGAGAGGATGATGATGATGATGATGATGATGATGATGAT 917
QY 946 AAAAGCCATGCGAGAGGAGGATGCTGCGAGCAGGATGATGATGATGATGATGATGATGATGAT 996
DB 918 ACCGTGAAGAAAGGATGTTGGACGAGACCTGAAGTCATGACAACTCCCATATTTAGGCA 977
QY 997 ----GCGAAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
DB 978 TGAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1037
QY 1053 ACAGACCAACAATATGCGCCAGCTCTTCATTAACATGCTGCTGCTGCTGCTGCTGCTGCT 1112
DB 1038 TGAGTGAGAACAAATGTAACCATTTTTCACAGCATGCTGCTGCTGCTGCTGCTGCTGCT 1097
QY 1113 TTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1172
DB 1098 ATGTTTACAGGAGCAAGATGTTGGCTCAGGACAAACGGGTAACGAGGAGGATGATTA 1157
QY 1173 TCATTCATGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1232
DB 1158 TCATTCATGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1217
QY 1233 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1292
DB 1218 AGATTTCTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1277
QY 1293 CCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1352
DB 1278 CCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1337
QY 1353 AGAGTGA 1359
DB 1338 GTTGCA 1344
RESULT 4
AF214106 1627 bp mRNA linear PLN 21-JUN-2000
LOCUS Arabidopsis thaliana farnesyltransferase beta subunit (ERAI) mRNA.
DEFINITION complete cds.
ACCESSION AF214106
VERSION AF214106.1 GI:8347239
KEYWORDS thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1627)
Ziegelhoffer,E.C., Medrano,L.J. and Meyerowitz,E.N.
Cloning of the Arabidopsis WIGGUM gene identifies a role for
farnesylation in meristem development
Proc. Natl. Acad. Sci. U.S.A. 97 (13), 7633-7638 (2000)
MEDLINE 20319078
REFERENCE 2 (bases 1 to 1627)
Ziegelhoffer,E.C., Medrano,L.J. and Meyerowitz,E.N.
Direct Submision
Submitted (09-DEC-1999) Biology, California Institute of
Technology, 1200 East California Boulevard, Pasadena, CA 91125, USA
FEATURES
source
1..1627
/organism="Arabidopsis thaliana"
/cultivar="Landsberg erecta"
/db_xref="taxon:3702"
/chromosome="5"
/map="15 Mb from top, between t12 and g13"
1..1627
/gene="ERAI"
/note="WIGGUM"
1..1449
/gene="ERAI"
/codon_start=1

```
/product="farnesyltransferase beta subunit"  
/protein_id="AAF74564.1"  
/db_xref="GI:8347240"  
/translation="MNVTRLLRLKCVGLRDLRSGINRIRICHGSESTRPRMELS  
SLTVSRDEPFLVNDVEFGIYTFEDASDVSTOKYMEIQROROLDYLMKGLRQLPDS  
SLDAMPFWLCTILHSLALIGETVDELSENATFLPGLCOSBEGVGQGLPHLAT  
TYAVNALVTLIGDALSSINREKMSCLRRMKPTSGFPRHMDGENDVACTAISV  
ASLNTIMDELTYGLADYILSCQYEGGIGEGSEAHGQYTCGLAAMLLINEVRL  
NLSLNNMAVHRQGVEMFQGRTNKLVQGCYTFQMAPCVLLQGLYSTNDHVDHGS  
ISEGTNEHHADDEDDLEDDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSD  
GLQRYVLCSSKIPDGGRFDRPKPRDFPDFTCYCSGLSVAGHMLKDEDTPPLTRD  
GYSNLEPVLQHLNHYMDQVNEALEFFKAA"  
BASE COUNT      453 a      310 c      393 g      471 t  
ORIGIN  
Query Match      31.3%; Score 424.8; DB 8; Length 1627;  
Best Local Similarity 59.1%; Pred. No. 1.2e-101;  
Matches 779; Conservative 0; Mismatches 512; Indels 27; Gaps 2;  
64 GACCTACCGGAGCTCAGGTGAGCGAGCGAGTGAAGTGGAGGCGAGGTTGGC 123  
124 GAGCTTTACAGCTTACCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 183  
124 GACATCTACCGCTCCCTCTTGGGGGCGGCCACACAGAAATCCATCATGAGC 183  
184 GCGATCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 243  
184 TGGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243  
244 CAGCGAGTAAAGCATTTGATTTATCTGATGAAGAGCTTAAAGCAGCTTGTC 303  
244 CATGTTCTAGATGAGCAATGCGCTTGGCTATGCTATGCTATGCTATGCTATG 303  
304 TCTTCCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 363  
304 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 363  
364 CTGGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 423  
364 CAGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 423  
424 CAGGCTCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 483  
424 TATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 483  
484 TATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 543  
484 AGGGCAACCTGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 543  
544 AGAGAAAAATGCTTGTGTTTTTAAGAGGATGAAGATGAAGATGAAGATGA 603  
544 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603  
604 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 663  
604 GTGATATATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 663  
664 CTAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 723  
664 ACTTATGAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 723  
724 ACTTATGAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 783  
724 TGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 843  
784 TGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 843  
844 ATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 903  
844 TTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 903
```

```
Db 904 TTGCTGATGCTGCTACATATTTTGGCAGGAGCCCTTGTGTTCTACTACAAAGATTA 963  
QY 904 ATTACGATTTGCTATGACAAATTAATTAATTAATTAATTAATTAATTAATTAAT 960  
Db 964 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1023  
QY 964 GAGCA-----TGCTGAGGAGCAAGTTTCAATGATGGTGAC 966  
Db 1024 GATCAATGCTATGATGAAGATGACCTTGAAGACGATGATGATGATGATGAT 1083  
QY 997 GCGAAAAAGTCTCTCTGCGGAGTATGACCAATTTGATGATGATGATGATGATG 1086  
Db 1084 GAGGACAAAGATGAAGATTAATGATGATGATGATGATGATGATGATGATG 1143  
QY 1057 AGCAACCAATTTGGCCCACTCTTCATTAATGATGATGATGATGATGATGATG 1116  
Db 1144 AACAGCAAAATGAAGATGATGATGATGATGATGATGATGATGATGATGATG 1203  
QY 1117 TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1176  
Db 1204 TCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263  
QY 1177 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1236  
Db 1264 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1323  
QY 1237 TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1296  
Db 1324 ACTGCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1383  
QY 1297 CCATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1354  
Db 1384 CTTCTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1441  
RESULT 5  
ATU44849  
LOCUS ATU44849 1331 bp mRNA linear PLN 02-FEB-1996  
DEFINITION Arabidopsis thaliana beta subunit of protein farnesyl transferase  
ACCESSION U44849  
VERSION U44849.1 GI:1174242  
KEYWORDS  
SOURCE  
ORGANISM  
thale cress.  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
1 (bases 1 to 1331)  
Culter,S., Ghasselman,M., Bonetta,D., Cooney,S. and McCourt,P.  
AUTHORS  
TITLE Direct Submission  
JOURNAL Submitted (08-JUN-1996) Majid Ghasselman, Botany, University of  
Toronto, 25 Wilcocks St. ESC room 4055, Toronto, Ont M5S 3B2,  
Canada  
FEATURES  
source  
CDS  
Location/Oualifiers  
1..1331  
/organism="Arabidopsis thaliana"  
/db_xref="taxon:3702"  
<1..1212  
/product="beta subunit of protein farnesyl transferase"  
/protein_id="AAF74564.1"  
/db_xref="GI:1174243"  
/translation="ETDRKQDLYLMKGLRQLPDSLDAMPFWLCTILHSLALIGETVDELSENATFLPGLCOSBEGVGQGLPHLAT  
TYAVNALVTLIGDALSSINREKMSCLRRMKPTSGFPRHMDGENDVACTAISV  
ASLNTIMDELTYGLADYILSCQYEGGIGEGSEAHGQYTCGLAAMLLINEVRL  
NLSLNNMAVHRQGVEMFQGRTNKLVQGCYTFQMAPCVLLQGLYSTNDHVDHGS  
ISEGTNEHHADDEDDLEDDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSD  
GLQRYVLCSSKIPDGGRFDRPKPRDFPDFTCYCSGLSVAGHMLKDEDTPPLTRD  
GYSNLEPVLQHLNHYMDQVNEALEFFKAA"  
BASE COUNT 388 a 253 c 311 g 379 t  
ORIGIN
```

Query Match	29.6%;	Score 402;	DB 8;	Length 1331;
Best Local Similarity	60.0%;	Pred. No. 1.3e-95;		
Matches 722;	Conservative	0;	Mismatches 455;	Indels 27;
				Gaps 2

Oy	178	GACCTGTGGCGTGAATCAGCAATTCGAAAGTATCGACGCGTGGCGTACAGGATATATGGACA	237
Db	1	GNACATTCACCCGAGATTAACCAATTCGATATATCTGATGCAAAAGCCTTAAGCGAGCTTGGTCCG	60
Oy	238	GCCCTTCATGTTCTAGATGCCAATCCGCCCTTGCTGATGCTACTGATGATGTTTCATCCACTT	297
Db	61	CAGTTTCTTCCCTTAGATAGCTAAATCGACACCTTGCTTCTCTGATGATCTTCTCATTCATTA	120
Oy	298	GCTTTCCTGATGAAGCAGCTGATGATGATCCTTGGATGATGATATCATAGACCTTCCTTAGCT	357
Db	121	GCTTTCCTTGGGAGACTGCTGATGATGATTAATGAAACCAATGCCATTCGATCTCTCTGGA	180
Oy	358	CGATGTCAGGATTAAGATGCGATTAATGCTGTGACCTGGACAGTTCCTCACCCTAGCT	417
Db	181	CGCTGCCAGCGCTCGAAGGCGATACGGTGGTGCCTCGCCCAACTTCGCACATCTTGGCA	240
Oy	418	ACGACCTATGCTGCTGTAATATACACTTGGTACAAATGAGGAGCAAAAGCATTTGTCATA	477
Db	241	ACTACTTATGCTGACGATGAATGACACTGTTTACTTTAGAGAGGTGACAAAGCCCTTCTTCA	300
Oy	478	ATCATATAGGGCAACCTGTACAAATTTTATGCTGCAGATGAAGAATGATACAGTGCCTTC	537
Db	301	ATTAAATAGAAAAAATGCTGCTGTTTTTAAGACGGATGAAAGGATACAACTGGAGGTTTC	360
Oy	538	ACAAATGCATGATGCGTGGGAAATGATATGTCCTGCTTCTACACCGCTATATGCTGGCC	597
Db	361	AGGATCATGATATGGGAAATGATGTTGTCGATGCTCACTACGCAATTTGCGTGA	420
Oy	598	AGCCTTGTGAATATTTCTTGATTTTAAACTCGCAAAAGGTGTAGCGCACTACATACGACA	657
Db	421	AGGATCTTAAATATATGAGATGATGAACCTACCCAGGGCTCTAGAGATTTACATCTTGAAT	480
Oy	658	TCTCAAACTTATGAAGTGGTATGCTGTGGGAGCCTTATGCTGAAGCACATGCTGGGTAT	717
Db	481	TGCCAAACTTATGAAGGGTGGATTTGGAGGGAAACCTGGCTCGAAGCTCAAGCTGGGTAT	540
Oy	718	ACATTCCTGATTTGCGCTGCTTGTGATTCCTGTTAATGAGCGACAGAAAGTTGACTTGCT	777
Db	541	ACCTACTGTGGTTTGGGCTATGATTTTAAATCAATGAGGTGACGCCCTTGGAAATTTGGAT	600
Oy	778	AGTTTATGCTGGCTGGTGGCTTTTTCGTCAAGAGAGTGCATCGGATTTCAACAGCAGCACT	837
Db	601	TCATTTATGAATTTGGGCTGTACATCGCAAGAGGTAGAATTTGGATTTCAAGGTAGSAG	660
Oy	838	AATTAATTTGCTGATGGTGTGCTACTCCTTTTGGCAGSAGCTGCGATTTGCTTTACACAA	897
Db	661	AACAATTTGCTGATGGTGTGCTACACATTTTGGCAGGAGGCCCTTGTGTTCTACTACAA	720
Oy	898	AACCTTAATACGATGTTGATTAAGCAATTTGAA---GTCCCTGTTTCTCTCAAAAGGCCA	954
Db	721	AGATTATATCAACCAATGATCANTGASAGCTTACATGATATACATATATGAAAGSAGCA	780
Oy	955	TCAGGAGAGA-----TGCCTCAGCACCACTTCAATATGCG	990
Db	781	ATATGAAGAATCATGATGCTATGATGAAGATGACCTTTGAAGCAACGATGATGATGAT	840
Oy	991	TGCACCGCCCAAAAGTCTCCCTGCGTGGAGCAATATGCGAAGTTTGGATTTGATTTTATA	1050
Db	841	TCGATGAGAGCAACGATGAAGATTCAGTGAAATGGTCAACAAATTCATCTACATCCAC	900
Oy	1051	CAAGACAGCAACCAATTTGGCCACTCTTCCATTAACATTTGCCCTGCACAAATCATCTTA	1110
Db	901	TACATTTAACGAGAAATGCAACTGGTTTTTGGATTACCTCGGCTTGCAGAGATATGTACTC	960
Oy	1111	CTTTGTTTCAGGTACTAGAGGGAGGCGCTGAGAGGTATGCGTAAGCAACAGATGAC	1170
Db	961	TTGTGCTTAAAGATTCCTCGAGGGTGGATTTCAAGCAAAAGCCGAGAAACCCGTGTACTTC	1020

[illegible]

[illegible]

RESULT 7	AR102373	2464 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR102373				
DEFINITION	Sequence 4 from patent US 6083917.				
ACCESSION	AR102373				
VERSION	AR102373.1	GI:12813171			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 2464)				
TITLE	Brown, M.S., Goldstein, J.L., Reiss, Y. and Marsters, J.				
JOURNAL	Methods and compositions for the identification, characterization				
FEATURES	and localization of farnesyltransferase				
source	Patent: US 6083917 A 04-JUL-2000;				
	Location/Qualifiers				
	1..2464				
	/organism="Unknown"				
BASE COUNT	556 a	705 c	630 g	573 t	
ORIGIN					

Query Match	15.28;	Score 206.6;	DB 6;	Length 2464;
Best Local Similarity	56.78;	Pred. No. 1.1e-43;		
Matches 402; Conservative	0;	Mismatches 304;	Indels 3;	Gaps 1;

[illegible][illegible]

```

RESULT 8
112220
LOCUS 112220 2464 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 4 from patent US 5420245.
ACCESSION 112220
VERSION 112220.1 GI:909718
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2464)
AUTHORS Brown,M.S., Goldstein,J.L. and Reiss,Y.
TITLE Tetrapeptide-based Inhibitors of farnesyl transferase
JOURNAL Patent: US 5420245-A 4 30-MAY-1995;
FEATURES
SOURCE
1. 2464
Location/Qualifiers
BASE COUNT 556 a 705 c 630 g 573 t
ORIGIN

```

Query Match	15.2%;	Score 206.6;	DB 6;	Length 2464;
Best Local Similarity	56.7%;	Pred. No. 1.1e-43;		
Matches 402; Conservative	0;	Mismatches 304;	Indels 3;	Gaps 1;

[illegible]

Db 385 AGCTGGAACTGCTAGATGAACCCATCCCGAGATAGTGGCTACAGATGTGTCTAGTTCC 444

Qy 352 TTAGCTGATGTAGAGATAAAGATGGTGGATATAGTGGTGGACTGGACAGTTGCTTCAG 411

Db 445 TTGGAGCTGTGTGACGAGCCGAGAGAGTAGGCTTTGGAGAGAGACCGGCTGATTCACAC 504

Qy 412 CTACCTACGACTTATCTCTGTAAATACACTTGTGCAATAAGGAGACGAAGGCATTG 471

Db 505 CTTCACCCACATATCAGCAGATCATGATGATTTGGCATTCATTCGACCGAGAGGCTTAT 564

Qy 472 TCATCATCAATGAGGGGCAACTGTACAAATTTATGCGAGAGAAAGATATATAGGT 531

Db 565 GACATCATTTAACGAGAAAGACTTCTCAGATTTTGTACTCCCTGAAGCAACTGACGGC 624

Qy 532 GCATTGCAAGATCAGTATGCTGGCGAAATGATGCCGTGCTTACACCCCTATATATG 591

Db 625 TCTTTTCTCATGATCTCGAGGTAGGAGTGTAGAGAAAGCGCATCTCTGCTGCTCG 684

Qy 592 GTTCCACGCTTGTGAATATCTTATTTTAAACGCGGCAAAAGGCTGAGCGCATCATATA 651

Db 685 GTACCCGTGAGCAACATCATCTCCAGACTCTTTTGAAGGCACTGCTGAATGGATA 744

Qy 652 GCAAGATGTAAACTTATGAAGTGTATGCTGTGGGAGCCCTTATGCTGAAGCACATGGT 711

Db 745 GCAAGGTGTAGAACTGTGGAAGGTGGCATGTGGGGGTACCAAGGATGAAAGCCCATGGT 804

Qy 712 GGGATATCAATCTGTGGATTTGGCTCTTTGATCTCGTCTTAATGAGGCAAGAACTTGA 771

Db 805 GGGATATCACTTCTGTGGCTGGCCCGCGGTGGTAATCCCAAGAGAGGAACCTTCTTGAAC 864

Qy 772 TTGCTCTGTTGATGTGGTGGGCTTTTGCTCA -- AGAGTGGAAATCGGATTTGCA 828

Db 865 TTGAAGAGCTTATTACAATGGGTGACAAACCGGACAGATGGCATTTTGAAGAGAGATTTTCA 924

Qy 829 GGAGCAACTATTAATTTGGTGTATGGTGTCTACTCTCTTTTGGCAG 874

Db 925 GGCCGCTGCAACAAGCTGGTGTAGTGGCTGTACTCTCTTTCAGAG 970

[illegible]

Db 328 AGCTTGAACTGCTAATGAAACCCATGCCAGTAAGTGGCTACAGATGTGTCTAGTTG 387

QY 352 TTAGCTGCATGTCAGATTAAGATGGTGGATATATGTGTGGACCTGGACATGGCTTAC 411

Db 388 CTGAGCTGTGTGACAGCCAGAAAGTGGCTTTGGAGAGAGACCCGGTCATATCCACAC 447

QY 412 CTAGCTACGACTTATCTGCTTAATATACATTGTGGCAATATAGGAGACGAAGAGCATTTG 471

Db 448 CTTCGACCCACATATGACGACGATCAATGCATTGTGCATCATTTGGACACCGGAGGGCTAT 507

QY 472 TCAATCATCAATATGGGGCACTGTACATTTTATGCTGCAGATGAAAGTGTATCAGT 531

Db 508 GACATCTATTACAGAGAGAGGCTTCTTAGATTAATTTGTACTCCCTGAGGCAACCTGCAGGC 567

QY 532 GCATTGGAATGCATGATGGTGGCCAAATTATATCTGGTCTTCTACACCCGCTATATAG 591

Db 568 TCTCTTTCTCATGCTGTGAGAGTGTAGTGTAGAGAGCCATATGTCTGGCTTC 627

QY 592 GTTCCCGACGCTTGTGAATTTCTTATTTTAACTGGCAAAAGSTGATGGCCATCTATA 651

Db 628 CTAGCCCTGGTGACACATCATCTACAGCTCTTTGAGGGCACTGCTGAATGGATA 687

QY 652 GCAAGATGTCAAACTTATGAGAGTGTATTGCTGGGAGCCCTTATGCTGAAGCATGT 711

Db 688 GCAAGGTGTGAGAACTGGGAAAGTGGCAATTTGGCGGGTACACAGAGATGAAAGCCATGGT 747

QY 712 GGGATATCAATTCGTGTGATGGCTCTCTTTGATCTCGTGTATATGAGGACAGAAACTTGC 771

Db 748 GGGTATACCTTCTGTGGCTGGCCGCGGTGGAATCTCAAGAGAGGAAAGCTTCTTGAC 807

QY 772 TTGGCTATGTTGATTTGGGCTGGGCTTTTGCTA ---AGAGTGGAAATGGGATTCGA 828

Db 808 TTGAGAGCTTATTACATATGGGTGACAAACCGGACGATGCGATTTTGAAGAGGATTTTCA 867

QY 829 GGACGAATTAATATGGTGTATGGTGTACTCTCTTTTGGCAG 874

Db 868 GGCGCGTGCACAAAGCTGGTGTATGGCTGTACTCTCTTGGCAGG 913

```

RESULT 12
HUMFTPTB      1582 bp      mRNA      1linear      PRI 12-JUN-1993
LOCUS         human farnesyl-protein transferase beta-subunit mRNA, complete cds.
DEFINITION    human farnesyl-protein transferase beta-subunit mRNA, complete cds.
ACCESSION     L00635
VERSION       L00635.1 GI:292032
KEYWORDS      farnesyl-protein transferase; farnesyl-protein transferase
              beta-subunit.
SOURCE        Homo sapiens placenta cDNA to mRNA.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 1582)
AUTHORS       Omer,C.A.
TITLE         Characterization of recombinant human farnesyl-protein transferase:
              cloning, expression, farnesyl diphosphate binding and functional
              homology with yeast prenyl-protein transferases
JOURNAL       Biochemistry (1993)
FEATURES
SOURCE        1. 1582
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /tissue-type="Placenta"
              20..1333
              /codon_start=1
              /product="farnesyl-protein transferase beta-subunit"
              /protein_id="AAA51854.1"
              /db_xref="GI:292033"
              /translation="MASPSFTTYCCPPSSSPVMSSEPLSLREFAHREKLDDSEYVT
              STEDAKVEKIOEVPSSIRKHLPLVLOREHREHYLRGLQDTDNYECLDASRYM
              LCVYIHLSELIDEPPIQIVATDVCQFLDCSPSGEGGCGQPHLAPLYAAVNL
              CIGTIEENYDILNREKLIQYISLKQPDGSFLMHVGEVDVNASCAVASALNITIT
              PLPEFGTAEWIAFCORNMGGIGVGPGEAHGVTGPGALAAVILIKRESNLSKSLDWM

```


Oy	412	CTACATACGACTATCTCTCTGTAAATACACTTGTGACATATAGGACCGCAAGACATTG	471
Db	463	CTTGCACCCACAAATATCCAGCATCAATTCATTTGGCATTCATGTGGCACCGGAGGCGTTAT	522
Oy	472	TCATCATCAATAGGGGCAACCTGTACAAATTTATATGCGAGATGAAGATGTATACAGT	531
Db	523	GACATCATTTAACGAGAGAAGCTTTCTTCAGTATTTGTATCTCCTGAAAGCAACCTGACGGC	582
Oy	532	GCTTTACGAATGCATGATGTTGGCGCAAAATGATGCCGTCTTCATCACCGCTATATCG	591
Db	583	TCCATTCTCATGATGATCCGAGGTAGGTGATGTGAAAGCGCATACTGCTGCTCC	642
Oy	592	GTTGCGACGCTTGTGAATTTCTTATTTTAACTGGCAAAAGGTGTAGGCGACTTCA	651
Db	643	GTACCTTCGCTGACACAACTATCACTCCAAACCTCTTTGGGGCACTGCTGATATGATA	702
Oy	652	GCAAGATGTCAAACTTATATGAGGTGATGCTGTGCTGGGAGCGTTATGCTGAAGCACATGT	711
Db	703	GCAAGGTGTACAACTGGGAGAGTGGCAATTTGGCGGGTACAGGAGTGAAGCCATGT	762
Oy	712	GGGATATCAATCTGTGTGATTTGGCTCCTTGTGATCTCGTTAATGAGCGACAGAAAGTTGC	771
Db	763	GGCTATACCTTCTGTGTGGCTGGCCCGCTGGTAAATCTCAAGAGGGAACCTTTCCTTGAAC	822
Oy	772	TTTGCTAGTTTGAATTTGGCTGGGTGCTTTTGCTCA--AGGATGGAATCCGATTTTCA	828
Db	823	TTGAAAGGCTTATTAACAATGGGTGACAAAGCGGAGATGGGATTTGAAGAGGATTTTCAG	882
Oy	829	GGACGAACATTAATATTTGGTGTATGATGGTTGCTACTCTCTTTTGGCAG	874
Db	883	GGCGCTGCMAAAGCTGGTGTATGGCTGATCAATCTCTTCCGACGG	928

412 CTACCTACGCACTTATGCTGCTGTAAATACACTTGTGACATAGGAGGCCAAGACATTG 471
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 298 CTTCCACCCCACTATGACAGCAAGTCAATGCATTGTGCATCATTTGGCACCGAGGACCTAT 357
 472 TCATCATCATTAATGGGGCAACCTGTACAAATTTTATGGTCGACGATGAAGTAATGTATCAGST 531
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 358 GACATCATTTAACAGAGAGAAAGCTTCTCAGTATTTTGTACTCCCTGAAGGCACCTGACGGC 417
 532 GCATTGCAAAATGCATGATGGTGGCGAAATTTGATGTCGTGCTTCACACCGCTATATATG 591
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 418 TCCTTTCTCATGATGTCGGAGGTAGGTGATGTGAAAGCATCTGCTGCTGCCTCC 477
 592 GTTCCACGCTTGTGAAATTTCTGATTTTAACTGGGCAAAAGTGTAGCCGACTACATA 651
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 478 GTACCTCGCTGACCAACATCATCACTCCAGACCTCTTTGGGGCACTGTGTATGGATA 537
 652 GCAGATGTCACAACTTATGAGGTGGTATTTGCTGGGGAGCCCTTATGCTGAAGCACAATGTT 711
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 538 GCAGGTGTGACAACTGGGAGAGTGGCATTTGGCGGGGGTACAGAGGATGGAAGCCATGTT 597
 712 GGGTATACATTCTGTGGATTGGCTGCTTTGATCCCTGCTTAATGAGGCAGAGAAAGTTGAC 771
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 598 GGGTATACCTTTCGTGTGGCTGGCCCGGCGGTGTAACTCTCAAGAGGAAACCTTCTTGAAC 657
 772 TTGGCTATGTTGATGGCTGGGGTGCGCTTTTGCTCA --- AGAGTGAATGCTGGATTTCAA 828
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 658 TTGAAGAGCTTATTACAAATGGGTGGACAAAGCCGGCAGATGCTATTTTGAAGAGAGATTTCAG 717
 829 GGCAGCACTAATAATTTGGTGTAGATGCTCTACTCTCTTTGGCAGG 874
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 718 GGGCGCTGGCAACAAGCTGGTGGATGGAGTGTACTCTCTTCTGGAGG 763

RESULT 14					
AR077273	AR077273	1248 bp.	DNA	linear	PAT 31-AUG-2000
LOCUS	Sequence 8 from patent US 5962243.				
DEFINITION	AR077273				
ACCESSION	AR077273.1	GI:10004019			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1248)				
TITLE	Brown,M.S., Goldstein,J.L. and James,G.L.				
JOURNAL	Methods for the identification of farnesyltransferase inhibitors				
FEATURES	Patent: US 5962243-A 8 05-OCT-1999;				
source	Location/Qualifiers				
	1..1248				
	/organism="unknown"				
BASE COUNT	286 a	339 c	338 g	285 t	
ORIGIN					

RESULT 15
 112222
 LOCUS 112222 1248 bp DNA linear PAT 26-JUL-1995
 DEFINITION Sequence 8 from patent US 5420245.
 ACCESSION 112222
 VERSION 112222.1 GI:909720
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 1248)
 AUTHORS Brown,M.S., Goldstein,J.L. and Reiss,Y.
 TITLE Telipeptide-based inhibitors of farnesyl transferase
 JOURNAL Patent: US 5420245-A 8 30-MAY-1995;
 FEATURES
 location/Qualifiers
 1..1248
 /organism="unknown"
 BASE COUNT 286 a 339 c 338 g 285 t
 ORIGIN

Query Match	14.7%	Score 200.4	DB 6	Length 1248
Best Local Similarity	55.2%	Pred. No. 4,10-42		
Matches 397	Conservative 0	Mismatches 306	Indels 3	Gaps 1
Qy	172	ATGCTAGAGCTGTGGCGGTATAGCATATCCAGTATCTGACGGCTTGAGGCATATG	231	
Db	58	AGGCTTGTTTTGGAGAGGAGCAAGCACTTCATATCTGAAAAGAGGCTTGGACACAGT	117	
Qy	232	GGACCAAGCTTTCATGTCTCTAGATGCCAATGGCCCTTGGCTACTTACTGATGGTTCA	291	
Db	118	ACAGATGCTATAGTGTCTGATGCCAGGCCCATATGGCTCTCTATTTAGTCCGAC	177	
Qy	292	CCACTTGCATTGCTGGATGAACACCTTANTGATGATCTTGGAATGATATCAGACTTC	351	
Db	178	AGCTTGGACCTGCTGAATATGACCCTCCACAGATAGGCTGTACAGCTGTGTCAAGT	237	
Qy	352	TTAGCTGATGTAGGATTAAGATGGTGGATATATAGTGTGACCTGGACAGTTGCCATC	411	
Db	238	CTGAGACTGTGTACAGCCCAAGATGTGGCTTTTGGAGAGGACCCGGCTGTATCCAG	297	

	Query Match	14.78	Score 200.4	DB 6	Length 1248
	Best Local Similarity	56.28	Pred. No. 4,1e-42		
	Matches 397	Conservative	0	Mismatches 306	Indels 3
				Gaps 1	
QY	172	ATGCTAGAGCTGCGCCGTGATGACGATATGCGAGTATCTGACGCGCTGGGCTGAGGCATATAG	231		
DB	58	AGGCTATTTTGGAGGAGGAGAAAGCATTCCTATATCTGAAAGAGGCTTCACACATCG	117		
QY	232	GGACCAACCCCTTCATGTTCTAGATGCCAATGCGCCCTTGCGATGCTCTACTGATGTTCTAT	291		
DB	118	ACAAATCCCTATACAGTCTGATGCCAGCCGCCCATGCGCTGCTTTTGATCCGCGAC	177		
QY	292	CCACTTCCTTGGTGATTAACCACTTGATGATGATCTTGGAAATCATATATACAGACTTC	351		
DB	178	AGCTGGAAATGCTTAATGAACCCATCCGCCGATAGGCGGTACAGATGTTGTCAGTTC	237		
QY	352	TTTACCTGATGTAGAGTAAAGATGATGATATATGATGACCTGGACAGCTGCCTAC	411		
DB	238	CTGAGAGTGTGTCAAGACCAGAAAGTGGCTTTGGAGAGAGACCCGGGTGATTCACAC	297		

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd

OM nucleic - nucleic search, using sw model

```
Run on: November 1, 2002, 12:10:44 ; Search time 252 Seconds
          (without alignments)
          9259.074 Million cell updates/sec
```

```

Title: US-09-786-675-11
Perfect score: 1359
Sequence: 1 atgagccctcccgagtc.....agttcttctcagaagatgta 1355

```

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

```
Searched:      1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Database : N_geneseq_572802.*

1:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
18:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24:	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1359	100.0	1339	21	AA251791	Corn farnesyltrans
2	613	45.1	1031	21	AA251792	Rice farnesyltrans
3	491.2	36.1	1504	21	AA251793	Soybean farnesyltr
4	426.4	31.4	1535	21	AA235019	Arabidopsis thalia
5	411.8	30.3	1525	21	AAC48831	Arabidopsis thalia
6	392.4	28.9	1356	21	AAC48830	Arabidopsis thalia
7	206.6	15.2	2464	15	AAO44398	Farnesyltransferas
8	206.6	15.2	2464	15	AAO94411	Rat farnesyl prote
9	206.6	15.2	2464	17	AA736709	Rat farnesyl trans

C	45	38.6	2.8	2842	21	AAAD00334	Rice raffinose synthase
C	44	38.6	2.8	1869	17	AAAT38712	Human GGTase-I beta
C	43	38.6	2.8	1969	16	AAO93111	Human GGTase-I beta
C	42	38.6	2.8	1670	15	AAO93111	Human GGTase-I beta
C	41	38.6	2.8	1670	16	AAO93111	Human GGTase-I beta
C	40	38.8	2.9	1422	22	AAAS41094	Soybean geranylgeranyl
C	39	39	2.9	5142	22	AAAD17756	Human Farnesyl transferase
C	38	39	2.9	77536	21	AAAI14651	Human Farnesyl transferase
C	37	39.6	2.9	423	18	AAAT80654	Human Farnesyl transferase
C	36	40.2	3.0	7346	20	AAZ51671	Human Farnesyl transferase
C	35	40.6	3.0	3946	20	AAZ58079	Human Farnesyl transferase
C	34	40.6	3.0	3946	20	AAZ58079	Human Farnesyl transferase
C	33	40.6	3.0	1975	20	AAZ28095	Human Farnesyl transferase
C	32	40.6	3.0	1662	20	AAZ31672	Human Farnesyl transferase
C	31	40.6	3.0	1662	20	AAZ38080	Human Farnesyl transferase
C	30	41.2	3.0	13613	21	AAZ87319	Human Farnesyl transferase
C	29	41.2	3.0	12441	21	AAZ87284	Human Farnesyl transferase
C	28	41.2	3.0	5970	21	AAZ56003	Human Farnesyl transferase
C	27	41.2	3.0	5970	21	AAZ56003	Human Farnesyl transferase
C	26	41.2	3.0	5970	21	AAZ56003	Human Farnesyl transferase
C	25	41.8	3.1	58073	18	AAAT58840	Human Farnesyl transferase
C	24	46.2	3.4	1411	22	AAAI1091	Human Farnesyl transferase
C	23	46.2	3.4	664	21	AAAF12707	Human Farnesyl transferase
C	22	49.2	3.6	1330	22	AAAF1093	Human Farnesyl transferase
C	21	58.6	4.3	3063	23	ABL26162	Drosophila melanogaster
C	20	59	4.3	3063	23	ABL26162	Drosophila melanogaster
C	19	60.8	4.3	1306	22	AAAG1092	Soybean geranylgeranyl
C	18	73.2	5.4	1293	21	AAAC35850	Arabidopsis thaliana
C	17	78.2	5.8	3175	21	AAAC37825	Arabidopsis thaliana
C	16	78.2	5.8	3175	21	AAAC37825	Arabidopsis thaliana
C	15	157.2	12.4	533	21	AAZ51794	Human Farnesyl transferase
C	14	157.2	12.4	533	21	AAZ51794	Human Farnesyl transferase
C	13	200.4	14.7	1248	17	AAAT38711	Human Farnesyl transferase
C	12	200.4	14.7	1248	17	AAAT38711	Human Farnesyl transferase
C	11	200.4	14.7	1248	17	AAAT38711	Human Farnesyl transferase
C	10	202	14.9	1314	15	AAO64888	Human Farnesyl transferase
C	9	202	14.9	1314	15	AAO64888	Human Farnesyl transferase
C	8	202	14.9	1314	15	AAO64888	Human Farnesyl transferase
C	7	202	14.9	1314	15	AAO64888	Human Farnesyl transferase
C	6	202	14.9	1314	15	AAO64888	Human Farnesyl transferase
C	5	202	14.9	1314	15	AAO64888	Human Farnesyl transferase
C	4	202	14.9	1314	15	AAO64888	Human Farnesyl transferase
C	3	202	14.9	1314	15	AAO64888	Human Farnesyl transferase
C	2	202	14.9	1314	15	AAO64888	Human Farnesyl transferase
C	1	202	14.9	1314	15	AAO64888	Human Farnesyl transferase

ALIGNMENTS

RESULT 1	
AA251791	
ID	AA251791 standard; cDNA; 1359 BP

DT 04-JUL-2000 (first entry)

Corn farnesyltransferase beta subunit cDNA

KM Corn; farnesyltransferase beta subunit; transgenic plant
KM drought tolerance; cell growth; ss.

05 Zea mays

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

PN WO200014207-A2

PD 16-MAR-2000

07-SEP-1999; 99WO-US20419

PR 08-SEP-1998; 98US-0099521

PA (DUPO) DU PONT DE NEMOURS & CO E.I.

PI	Cahoon	RE,	Miao G,	Powell W;
----	--------	-----	---------	-----------

XX

DR MPI: 2000-256964/22.
DR P-PSDB: AMV70502.
XX
PT New isolated polynucleotide encoding farnesyltransferase polypeptide is
PT useful for producing transgenic plants with an altered level of
XX farnesyltransferase -
XX
PS Claim 3: Page 38-39; 51pp; English.
XX
CC The present sequence is a cDNA encoding farnesyltransferase beta subunit
CC from clone p0127.cntbu.18r. Isolated from corn inbred tissue
CC cDNA library. The present sequence is used in the construction
CC of a chimeric gene to produce transgenic plants with altered level
CC of farnesyltransferase subunit. Plants with decreased farnesyltransferase
CC activity may have enhanced tolerance to drought stresses. Nucleic acids
CC encoding all or a part of farnesyltransferase proteins can be used in
CC studies to understand cell growth in plants and provide genetic tools to
CC control cell growth and improve tolerance to drought in mature plants.
XX
SO Sequence 1359 BP: 340 A: 308 C: 351 G: 360 T: 0 other:

Query Match 100.0%; Score 1359; DB 21; Length 1359;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1359: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGACCCCTCCCGCACTGAGCGCCGCCACGAGAGACCGCGGACGGCGCGAT 60
DB 1 ATGGACCCCTCCCGCACTGAGCGCCGCCACGAGAGACCGCGGACGGCGCGAT 60
OY 61 CCCGACCTACGAGAGCTGACGAGTGGAGAGATGAGTGGAGCCAGGCTT 120
DB 61 CCCGACCTACGAGAGCTGACGAGTGGAGAGATGAGTGGAGCCAGGCTT 120
OY 121 GCGGACATCTACCGCTCCCTCTTGGGGCCGCCACACGAAATCATCTAGTAG 180
DB 121 GCGGACATCTACCGCTCCCTCTTGGGGCCGCCACACGAAATCATCTAGTAG 180
OY 181 CTTGGCGGATGAGATGAGATGATCTGAGCGCTGGGTGAGATGAGAGACACC 240
DB 181 CTTGGCGGATGAGATGAGATGATCTGAGCGCTGGGTGAGATGAGAGACACC 240
OY 241 TTTTCATGTTTCTAGATGCGCAATCGCCCTGGCTATGCTACTGATGCTTCACTT 300
DB 241 TTTTCATGTTTCTAGATGCGCAATCGCCCTGGCTATGCTACTGATGCTTCACTT 300
OY 301 TTGCGGATGAGAGCACTGATGATCTTGAAGATGATATCTAATCTTACTCTGA 360
DB 301 TTGCGGATGAGAGCACTGATGATCTTGAAGATGATATCTAATCTTACTCTGA 360
OY 361 TGTGAGATTAAGATGATGATGATGAGACTGAGACAGTTGGCTCAGCTAGCTAG 420
DB 361 TGTGAGATTAAGATGATGATGATGAGACTGAGACAGTTGGCTCAGCTAGCTAG 420
OY 421 ACTTATGCTGCTGTAATATACACTTGTACAAATAGGAGAAAGACATTTGATCAATC 480
DB 421 ACTTATGCTGCTGTAATATACACTTGTACAAATAGGAGAAAGACATTTGATCAATC 480
OY 481 AATAGGGCAACCTGTACAAATTTATGCTGACATGAAGATGATGATGATGCTTTGAGA 540
DB 481 AATAGGGCAACCTGTACAAATTTATGCTGACATGAAGATGATGATGATGCTTTGAGA 540
OY 541 ATGCAATGATGCTGGGCAAAATGATGCTGCTTCTACACGCGCTATATCGTTGCCAGC 600
DB 541 ATGCAATGATGCTGGGCAAAATGATGCTGCTTCTACACGCGCTATATCGTTGCCAGC 600
OY 601 CTTGCAATATTTCTGATTTTAACTGGCAAAAGGTGTAGGCGAGTACATACAGATGT 660
DB 601 CTTGCAATATTTCTGATTTTAACTGGCAAAAGGTGTAGGCGAGTACATACAGATGT 660
OY 661 CAAACTTATGAAGGTGATGCTGGGAGACCTTATGCTGAAGACATGCTGGTATACA 720
DB 661 CAAACTTATGAAGGTGATGCTGGGAGACCTTATGCTGAAGACATGCTGGTATACA 720

OY 721 TTCTGTGATTTGGCTGCTTGTGATCTCTCTTATGAGGACAGAAAGTGTGCTGCTAGT 780
DB 721 TTCTGTGATTTGGCTGCTTGTGATCTCTCTTATGAGGACAGAAAGTGTGCTGCTAGT 780
OY 781 TTGATTTGCTGCTGCTGCTGCTTGTGATGAGAGATGAGATGAGATTTCAAGAGCAATAT 840
DB 781 TTGATTTGCTGCTGCTGCTGCTTGTGATGAGAGATGAGATGAGATTTCAAGAGCAATAT 840
OY 841 AATATGCTGATGCTGCTGCTGCTGCTTGTGATGAGAGATGAGATGAGATTTCAAGAGCA 900
DB 841 AATATGCTGATGCTGCTGCTGCTGCTTGTGATGAGAGATGAGATGAGATTTCAAGAGCA 900
OY 901 TTAATTTAGATTTGTTGATTAAGCAATGAGATGAGATGAGATTTCAAGAGCAATGAGCA 960
DB 901 TTAATTTAGATTTGTTGATTAAGCAATGAGATGAGATGAGATTTCAAGAGCAATGAGCA 960
OY 961 GAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 961 GAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
OY 1021 GACTATGCGAAGTTTGGATTTTATGCAACAGAGACCAAAATTTGGCCACTCTTC 1080
DB 1021 GACTATGCGAAGTTTGGATTTTATGCAACAGAGACCAAAATTTGGCCACTCTTC 1080
OY 1081 CATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 1081 CATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
OY 1141 AGGATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB 1141 AGGATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
OY 1201 GCGATTTACCGATGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
DB 1201 GCGATTTACCGATGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
OY 1261 CTTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 CTTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
OY 1321 AAGTACATACAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
DB 1321 AAGTACATACAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380

RESULT 2
AAZ51792 standard; cDNA: 1031 BP.
XX
AC AAZ51792;
XX
DT 04-JUL-2000 (first entry)
XX
DE Rice farnesyltransferase beta subunit cDNA.
XX
KW Rice; farnesyltransferase beta subunit; transgenic plant;
XX drought tolerance; cell growth; ss.
XX
OS Oryza sativa.
XX
PH Key Location/Qualifiers
FT 91..1029
FT CDS
FT /tag- a
FT /product- "Farnesyltransferase beta subunit"
FT /note- "Does not include stop codon"
XX
PN MO200014207-A2.
XX
PD 16-MAR-2000.
XX
PF 07-SEP-1999; 99MO-US20419.
XX

```

PR 08-SEP-1998; 98US-0099521.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E. I.
XX
XX Cahoon RE, Miao G, Powell W;
PI
DR WPI: 2000-256964/22.
XX P-PSDB; AAY70503.
XX
XX New isolated polynucleotide encoding farnesyltransferase polypeptide is
PT useful for producing transgenic plants with an altered level of
PT farnesyltransferase -
PT
PS Claim 3; Page 40-41; 51pp; English.
XX
XX The present sequence is a cDNA encoding farnesyltransferase beta subunit
CC from clone rlr24.pk0007.46 isolated from rice infected leaf
CC cDNA library rlr24. The present sequence is used in the construction
CC of a chimeric gene to produce transgenic plants with altered level
CC of farnesyltransferase subunit. Plants with decreased farnesyltransferase
CC activity may have enhanced tolerance to drought stress. Nucleic acids
CC encoding all or a part of farnesyltransferase proteins can be used in
CC studies to understand cell growth in plants and provide genetic tools to
CC control cell growth and improve tolerance to drought in mature plants.
XX
SQ Sequence 1031 BP; 228 A; 249 C; 302 G; 252 T; 0 other:

Query Match 45.1%; Score 613; DB 21; Length 1031;
Best Local Similarity 84.1%; Pred. No. 9.7e-180;
Matches 704; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

OY 57 GGATCCGACCTACCGAGCTGACGAGCGAGCGAGCATGAAGTGGAGGCCAG 116
DB 168 GCGCCGTGAGCTGCCCGGTGACTGTGACGAGGTGGAGCATGAAGTGGAGGCCAG 227
OY 117 GGTGGGACATCAACCGCTCCCTCGGGGGCGGCCCAACAGCAATTCATATCT 176
DB 228 GGTGGGACCAATTCACCGCTCCCTCGGGCAACGCCGCCCAATTCCTCATGTT 287
OY 177 AGAGCTGGCGGTGATGACATATCGATCTGAGCGCTGGCGTGAAGCATATGGAGCC 236
DB 288 AGAGCTGGCGGTGAGAGCATGTTGAGTATTTGACGAGAGGCGTGAACATCTTGGAGCC 347
OY 237 ACCCTTTCATGTTAGATGCAATCGCCCTGATGCTATGATGATGCTTCAATCCATC 296
DB 348 AAGCTTCATGCTGCTGATGCAATCGCACTTGGCTGTGCTACTGATTAATTCATGCACT 407
OY 297 TCGTTTGGTGGATGAAGCACTTGTATGATCTTGAGAAATGATATCATGACTTCTTACG 356
DB 408 TCGCTGTGTTGATGAATATACCTGACGATG---TTGAGGATGATATTTGTGACTTCTTATC 464
OY 357 TCGATGTGAGGATAAAGTGGTATATAGTGGTGAACCTGGCAATTCCTCCATCCTAGC 416
DB 465 TCGATGTGAGCAACAAGTGGTGTGTTGGCGGAGGACCTGGCAATTCCTCATCTGCG 524
OY 417 TACGACTTATCTCTGTTAAATATACCTTGTGACATATGAGGAGCGAAAGACATTGTCAATC 476
DB 525 TACAACCTATCTCTGTTAAATATACCTTGTACTATAGGAGAGGAAAGCGCACTATATC 584
OY 477 AATCAATATGGGACCGTATCAATTTTATGTCAGAGAAAGATGATGTCAGGCGTTT 536
DB 585 GGTAAACGAGCAACCGTATCAAGTTCATGCTTCGAGTGAAGATACATCGGAGCTTT 644
OY 537 CAGAAATGATATGCTGGCGAAATGATGTCCTGCTCCATACCCGCTATATGCGTTGC 596
DB 645 CAGAAATGATATGCTGGCGAAATGATGTCCTGCTCCATATACGCAATATCGGTTGC 704
OY 597 CAGCTTGTGAATATCTTGTGATTTAACTGCGCAAAAGGTGAGGATACATATGCAAG 656
DB 705 CAGCTTGTGAACATCTTGTGATGTTGAACAGCAAAAGGTGAGGAAATTCATATGAAC 764
OY 657 ATGTAAACCTATGAGGTGATGTTGCTGGGAGCCTTATGCTGAAGCAATGTTGGTA 716

```

```

DB 765 GTGTCAACCTATGAAGGTGSCATTGCTGGGAAACGTAATGCTGAAGCTCATGTGGGTA 824
OY 717 TACATTCGTGATGATGGCTGCTTATGATCCATGATGAGCGAGAAAGTGAATGCTGCC 776
DB 825 CACTTTTGTGGCTGCTGATGATGATCTTAAAGAGATGAGCAATGATGATTTGGC 884
OY 777 TAGTTTGAATGGCTGGTGGCTTTCTCAAGAGATGGAATGGGATTTCAAGAGCAAC 836
DB 885 TAGCTTGAATGGCTGGCGGATTTCCCAAGAGATGGAATGGGATTTCAAGAGCAAC 944
OY 837 TAATTAATTTGTTGATGTTCTTACTCTTTTGGCAGGAGCTGCATTTGCTTAC 893
DB 945 TAATTAATTTGTTGATGTTGTTCTTCTTTTGGCAGGAGCTGCTTCTTTAAC 1001

RESULT 3
AAZ51793
ID AAZ51793 standard; cDNA: 1504 BP.
XX
XX AAZ51793;
AC
XX 04-JUL-2000 (first entry)
DT
XX
DE Soybean farnesyltransferase beta subunit cDNA clone sfil.pk0086.h10.
XX
KM Soybean: farnesyltransferase beta subunit; transgenic plant;
XX drought tolerance; cell growth; clone sfil.pk0086.h10; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 63..1352
FT /tag= a
FT /product= "Farnesyltransferase beta subunit"
XX
PN WO200014207-A2.
XX
PD 16-MAR-2000.
XX
PF 07-SEP-1999; 99WO-US20419.
XX
PR 08-SEP-1998; 98US-0099521.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E. I.
XX
PI Cahoon RE, Miao G, Powell W;
DR
DR WPI: 2000-256964/22.
XX P-PSDB; AAY70504.
XX
PT New isolated polynucleotide encoding farnesyltransferase polypeptide is
PT useful for producing transgenic plants with an altered level of
PT farnesyltransferase -
PT
PS Claim 3; Page 42; 51pp; English.
XX
XX The present sequence is a cDNA encoding farnesyltransferase beta subunit
CC from soybean clone sfil.pk0086.h10.
CC The present sequence is used in the construction
CC of a chimeric gene to produce transgenic plants with altered level
CC of farnesyltransferase subunit. Plants with decreased farnesyltransferase
CC activity may have enhanced tolerance to drought stress. Nucleic acids
CC encoding all or a part of farnesyltransferase proteins can be used in
CC studies to understand cell growth in plants and provide genetic tools to
CC control cell growth and improve tolerance to drought in mature plants.
XX
SQ Sequence 1504 BP; 453 A; 298 C; 334 G; 419 T; 0 other:

Query Match 36.1%; Score 491.2; DB 21; Length 1504;
Best Local Similarity 61.8%; Pred. No. 8.8e-142;
Matches 815; Conservative 0; Mismatches 473; Indels 30; Gaps 1;

OY 70 CCGAGCTCAGCGTGCAGCGAGTGGAGCATGAAGGTGAGGCCAGGCTTGGCAGATC 129

```

[illegible]

Accession	Gene	Strain	Library	Reads	Contigs	Genes	Proteins	Functions
DB 1110	CAGGAGCAAGAGGGTGGACCTGACAGAGCAAAACCGCGTAAACGTAGAGATCATTTACACACA	1169						
QY 1180	TGCTACTGCTCCTCAGTGGCCCTCCGCAAGTTAGCCAGTACAGTGGCCATGACTGATCTGGTTCC	1239						
DB 1170	TGTTACTGTTTAAAGTGGACGCTCATATTGTGCGAATAGTTGGTCAACACCCAGATTC	1229						
QY 1240	TGCCCATTTACCTCAGCATGTGCTTGGACGCTACTCTAAATTTGCTGAGCCCAATCCATCCA	1299						
DB 1230	CCACACTGCGCTAAATCTAGATTAATAGGCCCGTACTCTAAATCTTAAAGCAACATCCAGCCC	1289						
QY 1300	CTCTACACATGTTGTTCCTACAGTAAAGTACCATACAGCCTATGAGTCTTCTTCAGAAAGAGT	1357						
DB 1290	CTCTTAATGTTGTTCTGGGACATATCGTAGGACTCATGAATTCCTTTACTGAGT	1347						
RESULT 4								
AAC35019	AAC35019 standard; DNA, 1525 BP.							
XX	AAC35019:							
AC	AAC35019:							
XX	AAC35019:							
XX	AAC35019:							
DT	17-OCT-2000 (first entry)							
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 8713.							
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 8713.							
XX	Hybridisation assay; genetic mapping; gene expression control;							
KM	protein identification; signal transduction pathway;							
KW	metabolic pathway; promoter; termination sequence; ss.							
XX	Arabidopsis thaliana.							
OS	Arabidopsis thaliana.							
XX	EPI033405-A2.							
PN	EPI033405-A2.							
XX	EPI033405-A2.							
PD	06-SEP-2000.							
XX	06-SEP-2000.							
PF	25-FEB-2000; 2000EP-0301439.							
XX	25-FEB-2000; 2000EP-0301439.							
PR	25-FEB-1999; 9905-0121825.							
PR	05-MAR-1999; 9905-0123180.							
PR	09-MAR-1999; 9905-0123548.							
PR	23-MAR-1999; 9905-0125788.							
PR	25-MAR-1999; 9905-0126264.							
PR	29-MAR-1999; 9905-0126785.							
PR	01-APR-1999; 9905-0127462.							
PR	06-APR-1999; 9905-0128234.							
PR	08-APR-1999; 9905-0128714.							
PR	16-APR-1999; 9905-0129845.							
PR	19-APR-1999; 9905-0130077.							
PR	21-APR-1999; 9905-0130449.							

PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140981.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145224.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.

PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150084.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159325.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161993.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match

31.4%; Score 426.4; DB 21; Length 1525;

Best Local Similarity 59.2% Pred. No. 1.2e-121:	
Matches 780; Conservative 0; Mismatches 511; Indels 27; Gaps 2;	
QY	64 GACCTACCGAGCCTCAGCGAGCGAGGTGGAGAGATAGACGTGAGCGCCAGCGTTGGC 123
Db	104 GAGCTTTAAACCCCTACACCGTGAAGTACACCGGACCAATTTCTGTGGAAGACATCTGTTTC 163
QY	124 GACATCTACCCCTCCCTCTTGGGGCCGCCACACGCAAAATCATCATGTGATAGCTG 183
Db	164 GCGATCTAATTAATCTTGAAGCGGAGGAGCTTTCTACGCAAAATACATGATGAGATTT 223
QY	184 TGGCCTGATCAGCATTCGATGATCTGAGCCCTGGGCTGAGGCATATGGAGCAGACTTT 243
Db	224 CAGCGAGATTAAGCAATGATGATTCGATGAAGAGCTTAAGGACCTTGGTCCGAGTTT 283
QY	244 CATGTTCTAGATGCCAATCGCCCTTGGCCTATCCCTACTGATGGATTCATCCACTTCTTG 303
Db	284 TCTTCCTTAGATGCAATCGACCTTGGCTTTGTACTGATTCCTTCATTCATACCTTTTG 343
QY	304 CTGATGAGAGCATTTGATGATCTTGAGATGATATATCATGACTTCTTAAGCTGATGT 363
Db	344 CTGGGAGACTGTGATGATGATTAAGAAAGCAATGCCATTCCTCTTGAGAGCTGC 403
QY	364 CAGATTAAGATGCTGATATAGTGTGACCTGACAGACTTCCCTACCTAGCTAGCTACT 423
Db	404 CAGGCTCTGAAAGGTGATAGCGGTGCTCCTGGCCAACTTCCACATCTTGCACACTACT 463
QY	424 TATGCTGCTGAATTAACACTTGTACATAGGAGCGAAGAGCATTTGTATCATCATCAT 483
Db	464 TATGCTGAGAGTAAGCACTTGTACTTTTGAAGGTGAGCAAAAGCCCTTCTTCAATTTAT 523
QY	484 AGGGCAACCTGTACAAATTTTATGCTGCAGATGAAGATGTATCAGTGCTCTTTCAGATG 543
Db	524 AGCGAAAAATCTCTGTTTATTTTAAAGCATGACATACAAAGAGAGTTCAGATG 583
QY	544 CATGATGCTGGGAAATTTGATGTCGCTGCTTCTACAGCGATATGCTTGGTCCGACCTT 603
Db	584 CATGATATGGAGAAATTTGATGTCGCTGCTTCTACAGCGATATGCTTGGTCCGACCTT 643
QY	604 GTGAATTTCTTGAATTTTAACTGGCAAAAGGTGAGGCGCATACATCAAGATGTCAA 663
Db	644 CTAAATATTAATGATGATGAACTCACCCAGGCGCTAGGATTAATCATCTTGAGTTGCCAA 703
QY	664 ACTTATGAAGTGTGATTTGGCGGGAGGCTTATGCTGAAGCAATGAGTGGGATATCATTC 723
Db	704 ACTTATGAAGTGTGATTTGGAGGGAGGAGCTGCTCGAAGCTCAGCGGGATACCTTAC 763
QY	724 TCTGATTTGGCTGCTTGTGATCTGCTTAATGAGGAGAGAAAGTTGACTTGGCTAGTTG 783
Db	764 TGTGTTTGGCTGCTTATGATTTTAAATGATGAGCTGACCGTTGAATTTGGATTCATTA 823
QY	784 ATTGCTTGGGGGCTTTTTCGCAAGAGCTGAGTGGGATTTCAAGGAGCAACTATATAA 843
Db	824 ATGAATTTGGGCTGTACATCGAAGAGAGTGAAGATGGATTTCAAGTGAAGAGCAAA 883
QY	844 TTGTTGATGCTTCTACTCCTTTTGGCAGGAGCTGCATTTGCTTTCACACAAAGTTA 903
Db	884 TTGCTGATGCTTCTACTACATTTTGGCAGGAGCCCTTGTGTTCTACTAAGAGATTA 943
QY	904 ATTACGATTTGTTGAAGCAATTGAA---GTCTCGTATTTCCGAAAAGGCCATCAGCA 960
Db	944 TATTCAACCATGATCATGAGCTTCATGATCATATATTCAGAAAGGCAAAATGAA 1003
QY	961 GAGCA-----TGCTGAGCAGACAGTTCAATGCTGACCC 996
Db	1004 GAAACATCATGCTCATGATGAAGATGACCTTGAAGACAGCATGATGATGATCTTGAT 1063
QY	997 GCGAAAAGCTTCTCCTCGCTGGAGTATGGAGATTTGGATTTGATTTTATACAAAG 1065
Db	1064 GAGGCAACGATGAAGATTAAGTGAATGTCAGAGAAATCATCATATACACTACTT 1123
QY	1057 AGCAACCAATTTGGCCAGCTTTCATACATTTGCCCTGCAAAATACATCTTACTTTGT 1116

Db	1124 AACAGAGATGCAAACTGTTTTTGTATAGCCTGGCTTGCAGAGATATGTACTCTTGTGC 1183
QY	1117 TCTCAGTACTAGAGGAGGCTGTGAGGATTAACCTCTGGAAGAAACAGATCATATCAT 1176
Db	1184 TTTAAGATCCCTGAGGCTGATTCAGAGCAACCCGAGAAACCCCGTACCTTACCCAC 1243
QY	1177 TCATGCTACTCCCTCAGTGGCTCGGAGTTAGCAGTACAGTGCCTAGTACTGATAGTGT 1236
Db	1244 ACATGTTACTCTGAGCGGCTTGTCTGTGGCTCAGCACGCTTGGTTAAAGAGAGGAC 1303
QY	1237 TGTGCCATTAATCTCAGCATGTGCTTGCACCTACTCTAATTTGCTGAGCCATTCAT 1296
Db	1304 ACTGCTCTTGTGACTGCGGACATTAATGCTGCTACTGCAATCTCTGAACCTGTTCAA 1363
QY	1297 CCAGTCTCAATGTTGTCTCAGTAAATACATACACCTATACATGCTTCTCAGAA 1354
Db	1364 CTCTTCAACATTTGTATGATGATGATTAATGAAGCATGATCTTCTTTAAAG 1421
RESULT 5	
AAC48831	
ID	AAC48831 standard; DNA; 1525 BP.
XX	
AC	AAC48831;
XX	
DT	18-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 58932.
XX	
KW	Hybridisation assay; genetic mapping; gene expression control;
KW	protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.
PR	19-APR-1999; 99US-0130077.
PR	21-APR-1999; 99US-0130449.
PR	23-APR-1999; 99US-0130510.
PR	23-APR-1999; 99US-0130891.
PR	28-APR-1999; 99US-0131449.
PR	30-APR-1999; 99US-0132048.
PR	30-APR-1999; 99US-0132407.
PR	04-MAY-1999; 99US-0132484.
PR	05-MAY-1999; 99US-0132485.
PR	05-MAY-1999; 99US-0132486.
PR	06-MAY-1999; 99US-0132487.
PR	07-MAY-1999; 99US-0132863.
PR	11-MAY-1999; 99US-0134256.
PR	14-MAY-1999; 99US-0134218.
PR	14-MAY-1999; 99US-0134219.
PR	14-MAY-1999; 99US-0134221.
PR	14-MAY-1999; 99US-0134370.
PR	18-MAY-1999; 99US-0134768.
PR	19-MAY-1999; 99US-0134941.
PR	20-MAY-1999; 99US-0135124.
PR	21-MAY-1999; 99US-0135353.
PR	24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142820.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145219.
PR 26-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.

PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148365.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149175.
PR 17-AUG-1999; 99US-0149368.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160914.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.

PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 30.38; Score 411.8; DB 21; Length 1525;
Best Local Similarity 59.08; Pred. No. 4.3e-117;
Matches 779; Conservative 0; Mismatches 512; Indels 30; Gaps 3;

OY 64 GACCTACCGGCTCAGCTGAGCGAGGTCAGATGAGTGGAGCCGAGGTCGC 123
DB 104 GAGCTTACAGCGCTACCGCTAGTCACGGGAGCAATTCGTGTGAGAGCAATGCTTC 163
OY 124 GACATCTACCCGCTCCCTTCCTGGGGCCGCCCAACAGCAATTCATGCTAGAGCTG 183
DB 164 GGGATCTTAATTAATCTTCGACGCGGAGGTTTCTACCAAAATACATGATGAGCAT 223
OY 184 TGGCGTGATGACATATGAGTATGAGCTGAGCGCTGGGCTGAGGATATGGAGCAGCTTT 243
DB 224 GAGCGAGATGACATGATGATATGATGATGATGATGATGATGATGATGATGATGAT 283
OY 244 CATGTTCTAGTCCCAATGCGCTTCGCTATGCTAGTGGATGCTGATGCTGCTTTG 303
DB 284 TCTTCCTTAGAGCTAACGACCTTGGCTTGTAGCTGATGATGATGATGATGATGATG 343
OY 304 CTGATGAGAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 363
DB 344 CTGGGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 403
OY 364 CAGGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 423
DB 404 CAGGCTCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 463
OY 424 TATGCTGCTGTAATTAACCTGTGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 483
DB 464 TATGCTGCTGTAATTAACCTGTGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 523
OY 484 ---AGGGGCAACGCTGACATTTTATGCTGACATGAGGAGGAGGAGGAGGAGGAGG 540
DB 524 AGCAG 583
OY 541 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 584 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 643
OY 601 CTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 644 ATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 703
OY 661 CAACTTATGAGAGTGGTATGCTGGGAGGCTTATGCTGAGAGCAATGCTGGTATACA 720
DB 704 CAACTTATGAGAGTGGTATGCTGGGAGGCTTATGCTGAGAGCAATGCTGGTATACA 763
OY 721 TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
DB 764 TACTGTGCTGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 823
OY 781 TTGATGCTGGGCTGCTGCTTTCGTAAGAGTGGATGCGGATTTTCAGAGCAATAT 840
DB 824 TTTAATGAATGGGCTGTAACACCAAGAGTGGATGCGGATTTTCAGAGCAATAT 883
OY 841 AAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
DB 884 AAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 943
OY 901 TTAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
DB 944 TTAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1003
OY 958 GAGAGAGA-----TGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 993
DB 1004 GAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1063
OY 994 ACCGGAAGAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1053

DB 1064 GATGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1123
OY 1054 CAGAGCAACCAATTTGGGCCACTTCTTCATTAACATTTGCCCTGCACAAATACATCTT 1113
DB 1124 ATTAACAG 1183
OY 1114 TCTTCTGAGTACTAG 1173
DB 1184 TCTTCTGAGTACTAG 1243
OY 1174 CATCTATCTATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1233
DB 1244 CACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1303
OY 1234 GCTTGGCCCATTAACATGAGATGATGATGATGATGATGATGATGATGATGATGATG 1293
DB 1304 GACATCTCTCTTGTAGCTCGGAGATTAATGAGGCTGCTGCTGCTGCTGCTGCTG 1363
OY 1294 CATCTATCTATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1353
DB 1364 CACTTCTTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1423
OY 1354 G 1354
DB 1424 G 1424

RESULT 6
AAC48830
ID AAC48830 standard; DNA: 1356 BP.
XX
AC AAC48830;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 58928.
XX
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 25-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130049.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136382.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148584.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154039.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0156599.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160960.
PR 22-OCT-1999; 99US-0160961.
PR 22-OCT-1999; 99US-0160969.

CC farnesyltransferase (FT) beta-subunit were determined. The cDNA
CC may be used to produce recombinant FT, useful for screening
CC potential anticancer agents that prevent expression of p21ras.
XX
XX
SO Sequence 2464 BP; 556 A; 705 C; 630 G; 573 T; 0 other:

Query Match 15.2%; Score 206.6; DB 15; Length 2464;
Best Local Similarity 56.7%; Pred. No. 3.4e-53;
Matches 402; Conservative 0; Mismatches 304; Indels 3; Gaps 1;

```

OY 172 ATGCTAGAGCTGTGGCGGATGACATATGATATGATGACGCTGGCTGAGCATATG 231
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 267 AGCGTCGTTCTGACAGAGGAGAACACTTCCATTATCTGAAAAGAGCCTTGACAACTG 326
OY 232 GAGCAGCGCTTTCATGTTCTAGATGCCCTTGGCTATGCTACTGATGATGCTTAT 291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 327 ACAGATGCTTATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 386
OY 292 CCACCTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 387 AGCTTGAGCTCTGACAGAACCCATCCCAATAGTGTGATGATGATGATGATGATGATG 446
OY 352 TTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 447 TTGAGAGCTGTGACAGAGTCCAGAGCTGCTTGGAGGGGCTGCTGATGATGATGATG 506
OY 412 CTAGCTAGCTTATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 507 CTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 566
OY 472 TCATCAATCAATAGAGGAGCACTGTACAAATTTATGCTGATGATGATGATGATGATG 531
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 567 AACGTCATTAACAGAGAGAGAGAGCTTCTGATGATGATGATGATGATGATGATGATG 626
OY 532 GCTTTCACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 627 TCTTTTTCATGACAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 686
OY 592 GTTGGCAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 651
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 687 GTAGCTCTTCTGACCAATATATATATATATATATATATATATATATATATATATAT 746
OY 652 GCAAGATGCAAACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 711
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 747 GCAAGGTGCAAGAACTGGGAGAGGGGATGATGATGATGATGATGATGATGATGATGATG 806
OY 712 GCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 771
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 807 GCGTACACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 866
OY 772 TTGCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 828
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 867 CTGAGAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 926
OY 829 GAGCAGCAATAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 877
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 927 GCGCTGCTGCAAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 975

```

RESULT 8
AA094411
ID AA094411 standard; DNA; 2464 BP.
XX

AC AA094411:

DT 23-JAN-1996 (first entry)

DE Rat farnesyl protein transferase gene beta subunit.

XX Farneyl transferase; inhibitor; cancer; ras; p21; ss.

OS Rattus sp.
XX

FH Key Location/Qualifiers
FT CDS 60..1373
FT */*tag= a*
FT */product= beta_farnesyl_transferase*

US5420245-A.
30-MAY-1995.
18-APR-1990; 90US-0510706.

16-JAN-1992; 92US-0822011.
18-APR-1990; 90US-0510706.
20-NOV-1990; 90US-0615715.
03-APR-1992; 92US-0863169.

(TEXA) UNIV TEXAS.

PI Brown MS, Goldstein JL, Reiss Y;

DR WPI: 1995-206308/27.

DR P-PSDB: AAR77840.

PT New farneyl transferase inhibitor peptide(s) - based on farneyl
PT acceptor substrate carboxy terminal sequences, used for the
PT treatment of cancer

PS Example 3; Column 53-56; 55pp; English.

CC AA094411 encodes the beta subunit of rat farneyl transferase which
CC is involved in the farneylation of various cellular proteins
CC including the cancer related ras proteins. It is used to produce the
CC complete farneyl transferase molecule which is used to demonstrate
CC the effectiveness of peptide inhibitors capable of inhibiting
CC farneyl transferases. The peptide inhibitors are useful for
CC treating cancers and ras-related cancers in particular.

SO Sequence 2464 BP; 556 A; 705 C; 630 G; 573 T; 0 other:

Query Match 15.2%; Score 206.6; DB 16; Length 2464;
Best Local Similarity 56.7%; Pred. No. 3.4e-53;
Matches 402; Conservative 0; Mismatches 304; Indels 3; Gaps 1;

```

OY 172 ATGCTAGAGCTGTGGCGGATGACATATGATGATGATGATGATGATGATGATGATG 231
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 267 AGCGTCGTTCTGACAGAGGAGAACACTTCCATTATCTGAAAAGAGCCTTGACAACTG 326
OY 232 GAGCAGCGCTTTCATGTTCTAGATGCCCTTGGCTATGCTACTGATGATGATGATGATG 291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 327 ACAGATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 386
OY 292 CCACCTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 387 AGCTTGAGCTCTGACAGAACCCATCCCAATAGTGTGATGATGATGATGATGATGATG 446
OY 352 TTAGCTGATGCTAGAGATTAAGATGTGATGATGATGATGATGATGATGATGATGATGATG 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 447 TTGAGAGCTGTGCAAGAGTGCAGAGGCTGTTTGAAGGGGCTGCTGATGATGATGATG 506
OY 412 CTAGCTAGCTTATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 507 CTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 566
OY 472 TCATCAATCAATAGAGGAGCACTGTACAAATTTATGCTGATGATGATGATGATGATG 531
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 567 AACGTCATTAACAGAGAGAGAGCTTCCATGATGATGATGATGATGATGATGATGATG 626
OY 532 GCTTTCACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 627 TCTTTTTCATGACAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 686
OY 592 GTTGGCAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 651
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Db 687 GTAGCCTCTCTCACCACATCATCACTCTGACCTTTGCAAGCAGCATGCTGATGATA 746
Qy 652 GCAAGATGCAACTTATGAGCTGTGATTCGCGGAGAGCTTATCTCAACACATAGT 711
Db 747 GCAGATGCGCAACACTGGGAAGATGCGGGGTGCGAGGATGAGAACCCACAGT 806
Qy 712 GGGTATACATTCGTGTGATGCGTCTTTGATCTGCTGATGAGGACAGAAAGTTGAC 771
Db 807 GCGTACACCTTCTGTGTGCTGTGCTGCTGATCTCTCAAGAACGACCTTTTGAC 866
Qy 772 TTGGCTAGTTTATGCTGGGTGGCTTTTGCTCA--AGAGTGGAAATGCGGATTTGCA 828
Db 867 CTGAGAGCTTCTCAATATGGGTACAAAGCGGACAGATGCGGTTGCAAGAGAGATTTGAG 926
Qy 829 GCACGAACTAATAATTGGTGTGATGCTGCTACTCTTTTGGCAGGAG 877
Db 927 GCCCGCTGCACACAGCTGTGTGAGCGCTGCTACTCTTCTGCGACGAC 975

RESULT 9
AAT38709
ID AAT38709 standard; cDNA: 2464 BP.
XX
AC AAT38709;
XX
DT 30-JUL-1997 (first entry)
XX
DE Rat farnesyl transferase enzyme beta subunit cDNA.
XX
KW Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;
KW ras protein; K-ras B; malignant; detection; identification; ss.
XX
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT CDS 59..1373
FT /tag= a
XX
PN W09634113-A2.
XX
PD 31-OCT-1996.
XX
PF 29-APR-1996; 96WO-US05969.
XX
PR 27-APR-1995; 95US-0429964.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Brown MS, Goldstein JL, James GL;
XX
DR WPI: 1996-497642/49.
DR P-PSDB: AAM04428.
XX
PT Assay for farnesyl transferase activity - by determining ability to
PT transfer farnesyl moiety to K-Ras B protein, partic. useful for
PT identifying inhibitors
XX
PS Example 3; Page 147-151; 257pp; English.
XX
CC AAT38709 encodes the beta subunit of a farnesyl transferase (FT) enzyme
CC derived from a rat brain cDNA library. The enzyme was used in a method
CC for identifying FT inhibitors. The method involved screening candidate
CC compounds for the ability to inhibit the transfer of a farnesyl moiety
CC to a K-ras B protein. FT inhibitors act by blocking the attachment of
CC prenyl groups to ras proteins in malignant cells of patients suffering
CC from cancer or precancerous states, and as such are used to treat such
CC conditions.
XX
SQ Sequence 2464 BP: 556 A; 705 C; 630 G; 573 T; 0 other;

Query Match 15.28; Score 206.6; DB 17; Length 2464;
Best Local Similarity 56.78; Pred. No. 3,4e-53;
Matches 402; Conservative 0; Mismatches 304; Indels 3; Gaps 1;

Qy 172 ATGCTAGAGCTGTGGCGTGAATCAGCATATGAGATATCTGACGCTGGCTGAGCATATG 231
Db 267 AGGCTGTCTGCAAGAGGAGAACCACTTCCATATCTGAAAGAGGCTTTCGAAACCTG 326
Qy 232 GGACGAGCTTTTCATATGTTCTAGATGCCAATCGCCCTTTGGCTATGCTACTGATGTTGAT 291
Db 327 ACAGATGCGCTATGATGCTGTGATGCCAGCCGCCCTGGCTGCTGCTACTGATGATCTGCAC 386
Qy 292 CCAGTTGCTTTGGCTGAGTGAAGCACTGATGATGATCTTGAAGATCATCTCACTACCTTC 351
Db 387 ACCTTGAGCTCTCTGAGAGAACCACTCCCAAAATGATGCTACAGATGTTGTCATTC 446
Qy 352 TTAGCTCATGTCAAGATTAAGATGTGATATAGTGTGAGCACTGAGCACTTGCTGCAC 411
Db 447 TTGGAGCTGTGTCAAGATCCAGAGCTGTGCTTTGAGGGGGCCCTGCTGATGATCCACAC 506
Qy 412 CTAGCTAGCACTTATGCTGTGTAATAACCTGTGTGACATAGGAGGCAAGAGCATTTG 471
Db 507 CTGCGTCCACGATATGACAGCTGTCAAGCGCTATGATCATTTGTGACAGAGAGAACCTAC 566
Qy 472 TCATCATATCATTAGGGCAACCTGTACAAATTTATGCTGCAGATGAAGATGTATCAGCT 531
Db 567 AACGTCAATTACAGAGAACAGCACTCTTCACTACTGTACTCCCTTAAGCAACCGGATGCG 626
Qy 532 GCTTTCAGAAATGATGATGCTGGGAAATGATGCTCGCTCTTCTACACCGCTATATCG 591
Db 627 TCTTTTCTCATGACAGCTGTGAGAGAGCTGTGATGTAAAGATGCTGCTACTGCTGCTCA 686
Qy 592 GTTGGCAGCTTGTGATATTTCTTGAATTTTAACTGGCAAAAGTGTGAGCACTACATA 651
Db 687 GTAGCCTCTCTCACCAATCATCATCTGTGACCTTTTGAAGCACTCTCAAAATGAGATA 746
Qy 652 GCAAGATGCAAACTTATGAGAGTGTATTTGCTGGGAGCGCTTATGCTGACACATAGT 711
Db 747 GCAAGTGCAGAACTGGGAAGGCGCATTTGGGGGTGCGAGGATGAGAACCCACGCT 806
Qy 712 GGGTATACATTCGTGTGATGCTGCTGCTTATGATCCTGCTTAATGAGGACAGAACTGAC 771
Db 807 GCGTACACCTTCTGTGTGCTGTGCTGCTGTGATCTCTCAAGAGAACGTTCTTTGAC 866
Qy 772 TTGGCTAGTTTATGCTGGGTGGGTGGCTTTTGCTCA--AGAGTGGAAATGCGGATTTGCA 828
Db 867 CTGAGAGCTTCTCAATATGGGTACAAAGCGGACAGATGCGGTTGCAAGAGAGATTTGAG 926
Qy 829 GCACGAACTAATAATTGGTGTGATGCTGCTACTCTTTTGGCAGGAG 877
Db 927 GCCCGCTGCACACAGCTGTGTGAGCGCTGCTACTCTTCTGCGACGAC 975

RESULT 10
AA064888
ID AA064888 standard; cDNA: 1314 BP.
XX
AC AA064888;
XX
DT 07-NOV-1994 (first entry)
XX
DE cDNA encoding beta subunit of human FRTase.
XX
KW Farnesyl protein transferase; inhibition; farnesylation; ss.
XX
OS Homo sapiens.
XX
PN W09410184-A.
XX
PD 11-MAY-1994.
XX
PF 29-OCT-1993; 93WO-US10442.
XX
PR 30-OCT-1992; 92US-0968782.
XX
PA (MERI) MERCK & CO INC.


```

FH Key Location/Qualifiers
FT CDS 1..1164
FT /tag= a
FT /note= "no start codon given"
XX
XX M09634113-A2.
XX
XX
XX
XX 31-OCT-1996.
XX
XX 29-APR-1996; 96MO-US05969.
XX
XX 27-APR-1995; 95US-0429964.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Brown MS, Goldstein JL, James GL;
XX
XX WPI: 1996-497642/49.
XX
XX P-PSDB: AAM04432.
XX
XX Assay for farnesyl transferase activity - by determining ability to
XX transfer farnesyl moiety to K-ras B protein, partic. useful for
XX identifying inhibitors
XX
XX Example 4; Page 161-163; 257pp; English.
XX
XX AAT38711 encodes the beta subunit of a farnesyl transferase (FT) enzyme
XX derived from a human retinal cDNA library. The enzyme was used in a
XX method for identifying FT inhibitors. The method involved screening
XX candidate compounds for the ability to inhibit the transfer of a
XX farnesyl moiety to a K-ras B protein. FT inhibitors act by blocking
XX the attachment of prenyl groups to ras proteins in malignant cells of
XX patients suffering from cancer or precancerous states, and as such are
XX used to treat such conditions.
XX
XX Sequence 1248 BP; 286 A; 339 C; 338 G; 285 T; 0 other:
SQ
Query Match 14.7%; Score 200.4; DB 17; Length 1248;
Best Local Similarity 56.2%; Pred. No. 1.9e-51;
Matches 397; Conservative 0; Mismatches 306; Indels 3; Gaps 1;
OY 172 ATGCTAGAGCTGGCGCTGATCAGATATCGAGTATCGACCGCTGGGCTGAGGCATATG 231
DB 58 AGGCTTTGTCAGAGGAGGAGGAGCACTTCATATCTGAAAAGAGGCGCTTCGACAACTG 117
OY 232 GGACGAGCCTTTCATCTTCTAGATGCCATCCGCTTGGCTATGCTACTGATGTTTCAT 291
DB 118 ACAATGCTATGATGCTGATGCGACCGCCATGCTCTCTATGATGATCCTGAC 177
OY 292 CCACCTTCCTTCTGATGAGCACTTGATGATCTTGAGATGATATCATAGACTTC 351
DB 178 AGCTTGGAACCTGATGAAACCCATCCCGAGATGAGTGTGTCAGTTC 237
OY 352 TTACTCTGATGTCGATTAAGATAGTGTGATAGTGGACCTCGACACTTGGCTTAC 411
DB 238 CTGAGAGCTGTGAGAGCCGAGAGGCTTTGGAGGAGGACCGGCTGATGATCCACAC 297
OY 412 CTACCTAGCACTTATGCTGCTGCTTAATACACTTGTGACAAATAGGAGGAGAAAGCATTTG 471
DB 298 CTTGACACCAATATGTCAGAGCATGATGTCATGTCATGTCGACGAGAGGCTTAT 357
OY 472 TCATCATCATAGGAGGCAACCTGTACAAATTTTATGCTCCGACAAATGAATGTATAGGT 531
DB 358 GACATCATTAACAGAGAAAGCTTTCTCAGTATTTTACTCCCTAGCAACCTGAGCGC 417
OY 532 GCTTTGCAATGATGATGCTGGCGAAATGATGTCCTGCTTCTTACACCGCTATATCG 591
DB 418 TCTTTTCTGATGATGTCGAGAGGTGAGGTGATGAGAAAGGCAATGCTGCTCCCTC 477
OY 592 GTTGGCAAGCCTTGATATATCTTGTATTTTAAAGCTGGCAAAAGGTGTAGCGACTACTCA 651
DB 478 GTAGCTGCTGACCAACATCATCTACTCCAGACCTCTTTGAGGCGACCTGCTGAATGATA 537

```

```

OY 652 GCAGATGTCAAACTTATGAAAGGTGGATTTGCTGGGAGACCTTATGCTGAAGCACATGGT 711
DB 538 GCAGAGTGTCAAGAACTGGGAAGGTGGATTTGGGAGGAGTACGAGGATGGAAGCCCATGGT 597
OY 712 GGGTATACATTTCTGTGGATTTGGCTGCTTTGATTCCTGCTTAATGAGCGACAGAAAGTTCAC 771
DB 598 GGTATACCTTCTGTGGCTGGCGGCTGGTATCTTCAGAGGAAAGCTTCTCCCTGAC 657
OY 772 TTGCCTAGTTGATGGCTGGTGGCTTTTCGCA---AGAGTGAATGGCGATTTCAA 828
DB 658 TTGAAGAGCTTATTAACATGGGTGACAGCCGGCAATGCTTATTTGAAAGAGATTTGAG 717
OY 829 GGAGCACTAATAATTTGTTGATGTTGCTACTCCTTTTGGCAGG 874
DB 718 GGCCGCTGCACAAAGCTGTGATGGCTGCTACTCTCTGCGCAGG 763

```

RESULT 14
AA064886
ID AA064886 standard; CDNA; 1314 BP.

AC AA064886;

DT 07-NOV-1994 (first entry)

DE CDNA encoding beta subunit of bovine brain FPTase.

XX Farnesyl protein transferase; Inhibition; farnesylation; ss.

XX Bos taurus.

XX W09410184-A.

XX 11-MAY-1994.

XX 29-OCT-1993; 93MO-US10442.

XX 30-OCT-1992; 92US-0968782.

XX (MERT) MERCK & CO INC.

XX Diehl RE, Gibbs JB, Kohl NE, Omer CA;

XX WPI: 1994-167373/20.

XX P-PSDB: AAR54829.

PT Mammalian farnesyl protein transferase prodn. - used in assays
PT for cDps. With inhibitory activity for the identification of
PT anticancer agents

XX Disclosure: Fig 1; 69pp; English.

CC The cDNA encoding the bovine beta subunit of FPTase was isolated
CC from a bovine brain oligo (dt) primed cDNA library in lambda gcl10
CC using a probe based on a fragment of the rat FPTase beta subunit.
CC The phrase can be used to isolate human FPTase sequences which can
CC be used to assess the inhibitory activity of a cpd. in the
CC farnesylation of a protein substrate. The assay can be used to
CC identify anticancer agents.
CC See also AA064887-9.

SQ Sequence 1314 BP; 289 A; 370 C; 372 G; 283 T; 0 other:

Query Match 14.7%; Score 199.2; DB 15; Length 1314;
Best Local Similarity 55.9%; Pred. No. 4.7e-51;
Matches 400; Conservative 0; Mismatches 313; Indels 3; Gaps 1;

```

OY 172 ATGCTAGAGCTGGCGCTGATCAGATATCGAGTATCGACCGCTGGGCTGAGGCATATG 231
DB 208 AGGCTTTGTCAGAGGAGGAGGAGCACTTCATATCTGAAAAGAGGCGCTTCGACAGCTG 267
OY 232 GGACGAGCCTTTCATGTTCTAGATGCCAATCGCCCTTGGCTATGCTAGTGAATGTTTCAT 291

```


Search completed: November 1, 2002, 13:36:04
Job time : 257 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: November 1, 2002, 13:31:59 ; Search time 56 seconds

(Without alignments)
5960.999 Million cell updates/sec

Title: US-09-786-675-11

Perfect score: 1359
Sequence: 1 atggaccctcccgagtc.....agttcttcagaaggtga 1359

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/2/lna/5A.COMB.seq:*
2: /cgn2_6/prodata/2/lna/5B.COMB.seq:*
3: /cgn2_6/prodata/2/lna/6A.COMB.seq:*
4: /cgn2_6/prodata/2/lna/6B.COMB.seq:*
5: /cgn2_6/prodata/2/lna/PCRTUS.COMB.seq:*
6: /cgn2_6/prodata/2/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206.6	15.2	2464	1 US-07-863-169A-4	Sequence 4, App11
2	206.6	15.2	2464	2 US-08-429-964-4	Sequence 4, App11
3	206.6	15.2	2464	3 US-07-935-087-4	Sequence 4, App11
4	206.6	15.2	2464	5 PCT-US93-08062-4	Sequence 4, App11
5	203.6	15.0	1413	3 US-07-935-087-8	Sequence 8, App11
6	202	14.9	1314	1 US-08-424-268-9	Sequence 9, App11
7	202	14.9	1314	5 PCT-US93-10442-9	Sequence 9, App11
8	200.4	14.7	1248	1 US-07-863-169A-8	Sequence 8, App11
9	200.4	14.7	1248	2 US-08-429-964-8	Sequence 8, App11
10	200.4	14.7	1248	5 PCT-US93-08062-8	Sequence 8, App11
11	199.2	14.7	1314	1 US-08-424-268-5	Sequence 5, App11
12	199.2	14.7	1314	5 PCT-US93-10442-5	Sequence 5, App11
13	197.2	14.5	2546	1 US-08-424-268-19	Sequence 19, App11
14	197.2	14.5	2546	5 PCT-US93-10442-19	Sequence 19, App11
15	59	4.3	1306	4 US-09-387-574-3	Sequence 3, App11
16	59	4.3	1306	4 US-09-668-096-3	Sequence 3, App11
17	49.2	3.6	1230	4 US-09-387-574-5	Sequence 5, App11
18	49.2	3.6	1230	4 US-09-668-096-5	Sequence 5, App11
19	46.2	3.4	1411	4 US-09-387-574-1	Sequence 1, App11
20	46.2	3.4	1411	4 US-09-668-096-1	Sequence 1, App11
21	41.2	3.0	1248	4 US-09-105-537-7	Sequence 7, App11
22	41.2	3.0	5970	3 US-09-320-878-21	Sequence 21, App11
23	40.6	3.0	13613	4 US-09-105-537-3	Sequence 3, App11
24	40.6	3.0	1659	4 US-09-083-351-3	Sequence 3, App11
25	40.6	3.0	1659	4 US-09-083-351-3	Sequence 3, App11
26	40.6	3.0	3946	3 US-09-083-351-1	Sequence 1, App11
27	40.6	3.0	3946	4 US-09-083-351-1	Sequence 1, App11

28	40.2	3.0	423	1 US-08-470-179-77	Sequence 77, App11
29	38.8	2.9	1422	4 US-09-387-574-7	Sequence 7, App11
30	38.8	2.9	1422	4 US-09-668-096-7	Sequence 7, App11
31	38.6	2.8	1670	1 US-08-189-772-10	Sequence 10, App11
32	38.6	2.8	1670	1 US-08-188-277B-5	Sequence 5, App11
33	38.6	2.8	1969	1 US-08-188-277B-3	Sequence 3, App11
34	38.6	2.8	1969	2 US-08-429-964-79	Sequence 79, App11
35	38.6	2.8	2913	1 US-08-188-277B-6	Sequence 6, App11
36	38.2	2.8	1187	1 US-08-440-856A-2	Sequence 2, App11
37	37.2	2.7	1365	4 US-09-319-892-1	Sequence 1, App11
38	36	2.6	1568	4 US-08-188-277B-1	Sequence 1, App11
39	36	2.6	1568	2 US-08-429-964-81	Sequence 81, App11
40	35.6	2.6	729	1 US-08-189-772-9	Sequence 9, App11
41	35.6	2.6	729	1 US-08-188-277B-26	Sequence 26, App11
42	35.2	2.6	68750	3 US-09-335-409-1	Sequence 1, App11
43	35.2	2.6	68750	4 US-09-568-102-1	Sequence 1, App11
44	35.2	2.6	68750	4 US-09-567-966-1	Sequence 1, App11
45	35.2	2.6	68750	4 US-09-568-480-1	Sequence 1, App11

ALIGNMENTS

```
RESULT 1
US-07-863-169A-4
; Sequence 4, Application US/07863169A
; Patent No. 5420245
;
GENERAL INFORMATION:
;
APPLICANT: BROWN, Michael S.
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: Tetrapeptide-based Inhibitors of Farnesyl
TITLE OF INVENTION: Transferase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
SERIAL: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/863,169A
FILING DATE: 03-APR-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/822,011
FILING DATE: 19-JAN-1992
CLASSIFICATION: 530
APPLICATION NUMBER: US 07/937,893
FILING DATE: 18-APR-1991
CLASSIFICATION: 530
APPLICATION NUMBER: US 615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 530
APPLICATION NUMBER: US 510,706
FILING DATE: 18-APR-1990
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:297/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
```

LENGTH: 2464 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-07-863-169A-4

Query Match 15.2%; Score 206.6; DB 1; Length 2464;
 Best Local Similarity 56.7%; Pred. No. 1.2e-53;
 Matches 402; Conservative 0; Mismatches 304; Indels 3; Gaps 1;

172 ATGCTAGAGCTGTGGCTGATCAGCATATGATATCTGACCGCTGGCTGAGCATATG 231
 267 AGGCTGCTTTCAGAGAGGAGAACACTTCAATTAATAAAGAGGCTTTCAGAACCTG 326
 233 GGACCAAGCTTTCATGTTCTAGATGCCAATCGCCCTTGGCTTACTGATGATGTTTCT 291
 327 ACAGATGCCATTGATGCTGTGATGCCAGCGCCCTGGCTGTCTGACTGATCTCTGCAC 386
 292 CCACCTTCTTGTCTGATGAAAGCACTTGATGATGATCTGAGAAATGATATCATAGACTTC 351
 387 ACCTTGGAGCTCTCGAGAACCCATCCCAATAGTGGCTACAGATGCTGTCTGACTTC 446
 352 TTAGCTCATGTCAGATTAAGATGTGATAGTGTGAGACCTGGACAGTTGCCCTCAC 411
 447 TTGAGAGCTGTGTCAAGAGTCCAGACGCTGGCTTTGAGAGGGGGCCCTGGTCACTACAC 506
 412 CTAGCTAGCACTTATGCTGCTTAATAACACTTGTGACAAATAGGAGCGAAGACATTTG 471
 507 CTCGCTCCACAGTATGACAGCGCTATGATGATGATGATGATGATGATGATGATGATG 566
 472 TCATCAATCAATAGGGGCAACCTGTACAAATTTATGCTGCAGATGAAAGATGTATCAGCT 531
 567 AACGTCAATTAACAGAGAGAACCTCTTCACTACTGTACTCTTAAAGCAACCGATGGC 626
 533 GCTTTCACAAATGCAATGATGGTGGGAAATGATGATGATGATGATGATGATGATGATG 591
 627 TCTTTTTCATGACAGCTGCGAGAGAGAGTGAATGAAGATGCGCTGCTGCTCCCTCA 686
 592 GTTGGCAGCCTGTGATATTTTCTGATTTTAACTGCAAAAGGTGTAGCGCATACATA 651
 687 GTACGCTCTCTACCAACATCATCATCTGACCTCTGCAAGGCACTCTGATGATGATA 746
 652 GCAAGATGCAACTTATGAAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 711
 747 GCAAGCTCCCAAGCTGGAGAGGGGATGAGGGGATGAGGGGATGAGGGGATGAGGGGAT 806
 712 GGGTATACATTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
 807 GGCCTACACTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 866
 772 TTGCTACTTTGATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 828
 867 CTGAAGAGCTTCTGCTACATGAGGTGACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 926
 829 GGACCAACTAATAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 877
 927 GGCCGCTCAACAGCTGTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 975

RESULT 2

US-08-429-964-4
 Sequence 4, Application US/08429964

Patent No. 5962243
 GENERAL INFORMATION:
 APPLICANT: BROWN, MICHAEL S.
 APPLICANT: GOLDSTEIN, JOSEPH L.
 APPLICANT: REISS, GUY L.
 APPLICANT: JAMES, GUY L.
 TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ARNOLD, WHITE & DURKEE

STREET: P. O. BOX 4433
 CITY: HOUSTON
 STATE: TEXAS
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/429,964
 FILING DATE: 27-Apr-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/021,625
 FILING DATE: 16-Feb-1993
 CLASSIFICATION: 435
 APPLICATION NUMBER: US 07/822,011
 FILING DATE: ABANDONED
 CLASSIFICATION: 435
 APPLICATION NUMBER: PCT/US/91/02650
 FILING DATE: 18-Apr-1991
 CLASSIFICATION: 435
 APPLICATION NUMBER: US 07/615,715
 FILING DATE: 20-Nov-1990
 CLASSIFICATION: 435
 APPLICATION NUMBER: US 07/510,706
 FILING DATE: 18-Apr-1990 (ABANDONED)
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PARKER, DAVID L.
 REGISTRATION NUMBER: 32,165
 REFERENCE/DOCKET NUMBER: UTSD:432/PAR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (713) 789-2679
 TELEX: 79-0924
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2464 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-429-964-4

Query Match 15.2%; Score 206.6; DB 2; Length 2464;
 Best Local Similarity 56.7%; Pred. No. 1.2e-53;
 Matches 402; Conservative 0; Mismatches 304; Indels 3; Gaps 1;

172 ATGCTAGAGCTGTGGCTGATCAGCATATGATATCTGACCGCTGGCTGAGCATATG 231
 267 AGGCTGCTTTCAGAGAGGAGAACACTTCAATTAATAAAGAGGCTTTCAGAACCTG 326
 233 GGACCAAGCTTTCATGTTCTAGATGCCAATCGCCCTTGGCTTACTGATGATGTTTCT 291
 327 ACAGATGCCATTGATGCTGTGATGCCAGCGCCCTGGCTGTCTGACTGATCTCTGCAC 386
 292 CCACCTTCTTGTCTGATGAAAGCACTTGATGATGATGATGATGATGATGATGATGATGAT 351
 387 ACCTTGGAGCTCTCGAGAACCCATCCCAATAGTGGCTACAGATGTGTGCTGACTTC 446
 352 TTAGCTCATGTCAGATTAAGATGTGATAGTGTGAGACCTGGACAGTTGCCCTCAC 411
 447 TTGAGAGCTGTGTCAAGAGTCCAGACGCTGGCTTTGAGAGGGGGCCCTGGTCACTACAC 506
 412 CTAGCTAGCACTTATGCTGCTTAATAACACTTGTGACAAATAGGAGCGAAGACATTTG 471
 507 CTCGCTCCACAGTATGACAGCGCTATGATGATGATGATGATGATGATGATGATGATGATG 566
 472 TCATCAATCAATAGGGGCAACCTGTACAAATTTATGCTGCAGATGAAAGATGTATCAGCT 531
 567 AACGTCAATTAACAGAGAGAACCTCTTCACTACTGTACTCTTAAAGCAACCGGATGGC 626

STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK/ASKII
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08062
FILING DATE: AUGUST 24, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/935,087
FILING DATE: 24 AUGUST 1992 (24.08.92)
NAME: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTPD377PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US93-08062-4

Query Match 15.2%; Score 206.6; DB 5; Length 2464;
Best Local Similarity 56.7%; Pred. No. 1.2e-53;
Matches 402; Conservative 0; Mismatches 304; Indels 3; Gaps 1;

QY 172 ATGCTAGAGCTGTGGCGTGTATGACATATGATGAGCGCTGGCGTGGCATATG 231
DB 267 AGCGTCGTTCTGCGAGAGGAGAACACTTCATTATCTGAAGAGCGCTTGACAACTG 326
QY 232 GGACGACGCTTTCATGTTCTGATGCCATCGGCCCTGGCTAGTACTGATGATGTTTAT 291
DB 327 ACAGATGCGCTATGATGCTGTGATGCCAGCCGCCCTGGCTGCTACTGATGCTGCAC 386
QY 292 CCAGTTCCTTGGCTGATGAGCAAGCACTGATGATCTTGACAAATGATATGATGATG 351
DB 387 ACCTTGGAGCTCTGAGAGAACCCCATCCCCAAATAGTGCTACAGATGTGTGAGTTG 446
QY 352 TTAGCTGATGTCAGAGTAAGATGTGATATAGTGTGAGACCTGGACACTTGGCTGAC 411
DB 447 TTGGAGCTGTGACAGAGTCCAGAGGTGGCTTTGGAGGGGCCCTGTGATGATGATGATG 506
QY 412 CTAGCTAGCACTTATGCTGCTGTAATATACACTTGTGACAAATGAGGAGCGAAGACAT 471
DB 507 CTGGCTCCAGTGTGACAGCTGTAACGCGCTATGATGATGATGATGATGATGATGATG 566
QY 472 TCATCAATCAATAGGCGCAACCTGTACAAATTTATGCTGACAGTGAAGATGATGATG 531
DB 567 AACGTCATTTAAGAGAGAGAGCTCTCACTACTTACTTACTTACTTACTTACTTACTT 626
QY 532 GCTTTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591
DB 627 TCTTTTTCATGACAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 686
QY 592 GTTGGACAGCTTGTGAATATTTGATTTTAACTGGCAAAAGGTGTAGCGCACTACATTA 651
DB 687 GTAGGCTCTCTCAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 746
QY 652 GCAAGATGTCAAACTTATGAAGGTGATGATGATGATGATGATGATGATGATGATGATG 711
DB 747 GCAAGGTCCAGAACTGGAGAGCGGCAATTTGGGGGTGCCAGGATGCAAGCCACCGT 806

QY 712 GGCTATACATCTGTGATGATGCTGTTGATCTCTGCTTAATGAGGACAGAAAGTGTAC 771
DB 807 GGCTACACCTTCTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 866
QY 772 TTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828
DB 867 CTGAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 926
QY 828 GGACGACCTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 877
DB 927 GGCCGCTGCAACAGCTGTGAGAGGCTGCTACTTCTTCTGCGAGGACG 975

RESULT 5
US-07-935-087-8
Sequence 8, Application US/07935087
Patent No. 6083917
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: THE IDENTIFICATION,
TITLE OF INVENTION: CHARACTERIZATION,
TITLE OF INVENTION: AND INHIBITION OF PARNESYL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: ARNOLD, WHITE & DURREE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1 (converted to ASCII-DOS)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/935,087
FILING DATE: 19920824
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/822,011
FILING DATE: 01/16/92
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:269/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1413 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-935-087-8

Query Match 15.0%; Score 203.6; DB 3; Length 1413;
Best Local Similarity 56.5%; Pred. No. 7.1e-53;
Matches 399; Conservative 0; Mismatches 304; Indels 3; Gaps 1;

QY 172 ATGCTAGAGCTGTGGCGTGTATGACATATGATGAGCGCTGGCGTGGCATATG 231
DB 265 AGCGTCGTTTCTGCGAGAGGAGAACACTTCATTATCTGAAGAGCGCTTGACAACTG 324
QY 232 GGACGACGCTTTCATGTTCTGATGCCAATCGCCCTTGGCTAGTACTGATGATGATGAT 291

APPLICANT: Omer, Charles A
APPLICANT: Diehl, Ronald B
APPLICANT: Gibbs, Jackson B
APPLICANT: Kohl, Nancy E
TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
TRANSFERASE
NUMBER OF INVENTION: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10442
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/968,782
FILING DATE: 10/30/92
ATTORNEY/AGENT INFORMATION:
NAME: Mulhard, David A
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18858
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOHETICAL: NO
ANTI-SENSE: NO
PCT-US93-10442-9

Query Match 14.9%; Score 202; Length 1314;
Best Local Similarity 56.4%; Pred. No. 2, 1e-52;

Matches 398; Conservative 0; Mismatches 305; Indels 3; Gaps 1;

QY 172 ATGCTAGAGCTGTGGCGTGCATGACCATATGAGATCTGACGCTGGCTGAGCATATG 231
DB 208 AGCGTTGTTTGCAGAGGAGAACCCATTTCATATCTGAAAGAGGCCCTTGACAACTG 267
QY 232 GGACCAAGCTTTCATGTTCTAGATGCCATCGCCCTTGCTATGCTACTGATGGTTCAT 291
DB 268 ACAGATGCGTATGATGTCGTGATGCGAGCGCCCATGGCTGCTGATTTGATTCCTGCAC 327
QY 292 CCACCTTCTTCTGTGATGAGACGCTGATGATGATCTTGAGATATTCATTAACCTTC 351
DB 328 ACCTTGGAAGCTCTAGATGAGAACCCATCCCGCATAGTGGTCAACAATCTGTCTAGTTC 387
QY 352 TTACCTGATGTCAGATGAAGATGATGATATAGTGTGACCTGACGATTTGCTCAG 411
DB 388 CTGGAGCTGTGACAGAGCCAGAGGTGGCTTTGGAGAGAGACCCGCTGAGTATCCACAC 447
QY 412 CTAGCTAGCACTTATCTGCTGTAAATACACTTGTGACAAATAGGAGCGCAAGACATTG 471
DB 448 CTTGAGACCATATATGACGAGTCAATGTCATCTTGGCACCAGAGAGCCCTAT 507
QY 472 TCATCAATCAATAGGGGCAACCTGTACAAATTTATGCTGAGATGAAAGATGATACAGT 531
DB 508 GACATCATTTAACAGAGAGACCTTCTTCAATTTTGTACCTCTGAGACAACTGACCGC 567
QY 532 GCTTTCAGATGATGATGTGGCGAAATGATGTCCGTCTTCTCAACCCCTATATCG 591
DB 568 GCTTTCAGATGATGATGTGGCGAAATGATGTCCGTCTTCTCAACCCCTATATCG 591

DB 568 TCCCTTTCATGATGTCGAGGTGAGTGTGATGAGAGGACGATCTGCTCCCTTC 627
QY 592 GTTCCAGCCTTGTGATATATTTTAACTGGCAAAAGTGTAGCGCATACATA 651
DB 628 GTAGCTGCTGACCAACATCATCATCCAGACCTTTTGGAGGGCACTGCTGAAGGATA 687
QY 652 GCAGATGTCAAACTTATGAGAGGTATGCTGGGAGACCTTATTCCTGAACACATGCT 711
DB 688 GCAAGTGTCAAGACTGAGGAAGTGTGATGGGGGTACACAGGATGGAAGCCCATGCT 747
QY 712 GCGTATACCTTGTGATGATGGCTGCTTTGATCTCTTAATGAGGACAGAAAGTTGAC 771
DB 748 GCGTATACCTTGTGATGATGGCTGCTTTGATCTCTTAATGAGGACAGAAAGTTGAC 807
QY 772 TTGCTTATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
DB 808 TTGAGAGCTTATTAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 867
QY 828 GGACCAACTAATTAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 874
DB 868 GCGCTGCTGCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 913

RESULT 8
US-07-863-169A-8
Sequence 8, Application US/07863169A
Patent No. 5420245
GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: Tetrapeptide-Based Inhibitors of Farnesyl
TRANSFERASE
NUMBER OF INVENTION: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/863,169A
FILING DATE: 03-Apr-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/822,011
FILING DATE: 19-Jan-1992
CLASSIFICATION: 530
APPLICATION NUMBER: US 07/937,893
FILING DATE: 18-Apr-1991
CLASSIFICATION: 530
APPLICATION NUMBER: US 615,715
FILING DATE: 20-Nov-1990
CLASSIFICATION: 530
APPLICATION NUMBER: US 510,706
FILING DATE: 18-Apr-1990
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: US/07/297/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 789-2679
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 1248 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-863-169A-8

Query Match 14.7%; Score 200.4; DB 1; Length 1248;
Best Local Similarity 56.2%; Pred. No. 6.4e-52;
Matches 397; Conservative 0; Mismatches 306; Indels 3; Gaps 1;

OY 172 ATGTAGAGCTGGCGCGTATGACATGACATGACCCCTGGGCTGAGGACATG 231
DB 58 AGCGTTGTTTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 117
OY 232 GGACAGCGCTTTCATGTTCTAGATGCAATCGCCCTTGCTAGTCTGATGATG 291
DB 118 ACAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 177
OY 292 CCAGTGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 351
DB 178 AGCTTGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 237
OY 352 TTAGCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 411
DB 238 CTGAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 297
OY 412 CTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 471
DB 298 CTGAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 357
OY 472 TCATCATCAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 531
DB 358 GACATCATTAACAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
OY 532 GCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591
DB 418 TCCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
OY 592 GTTCCAGCGCTTTCATGATGATGATGATGATGATGATGATGATGATGATG 651
DB 478 GTAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 537
OY 652 GCAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 711
DB 538 GCAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 597
OY 712 GGGTATACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 771
DB 598 GGGTATACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 657
OY 772 TTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 831
DB 658 TTGAGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 717
OY 839 GAGCAACTAATAATGATGATGATGATGATGATGATGATGATGATGATGATG 898
DB 718 GCGCGCTGCAACAGCTGATGATGATGATGATGATGATGATGATGATGATG 773

RESULT 9
US-08-429-964-8
Sequence 8, Application US/08429964

Patent No. 5962243
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REISS, YUYAL
APPLICANT: JAMES, GUY L.
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
TRANSFERASE INHIBITORS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DUKREE

STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,964
FILING DATE: 27-APR-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,625
FILING DATE: 16-FEB-1993

CLASSIFICATION: 435
APPLICATION NUMBER: US 07/822,011
FILING DATE: ABANDONED

CLASSIFICATION: 435
APPLICATION NUMBER: PCT/US/91/02650
FILING DATE: 18-APR-1991

CLASSIFICATION: 435
APPLICATION NUMBER: US 07/615,715
FILING DATE: 20-NOV-1990

CLASSIFICATION: 435
APPLICATION NUMBER: US 07/510,706
FILING DATE: 18-APR-1990 (ABANDONED)

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:432/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679

TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1248 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-429-964-8

Query Match 14.7%; Score 200.4; DB 2; Length 1248;
Best Local Similarity 56.2%; Pred. No. 6.4e-52;
Matches 397; Conservative 0; Mismatches 306; Indels 3; Gaps 1;

OY 172 ATGTAGAGCTGGCGCGTATGACATGACATGACCCCTGGGCTGAGGACATG 231
DB 58 AGCGTTGTTTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 117
OY 232 GGACAGCGCTTTCATGTTCTAGATGCAATCGCCCTTGCTAGTCTGATGATG 291
DB 118 ACAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 177
OY 292 CCAGTGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 351
DB 178 AGCTTGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 237
OY 352 TTAGCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 411
DB 238 CTGAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 297
OY 412 CTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 471
DB 298 CTGAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 357
OY 472 TCATCATCAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 531
DB 358 GACATCATTAACAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417

```

0Y 532 GATTTCAGAAATCATGATGTGGTGGCGAATTGACCTGCCTCCACACCGCTAATATAC 591
Db 418 TCCCTTTTCATCAGTCATGTGGAGTGTAAGTGTGATGTATGAGAAGGCCACTACTGTCTCC 477
0Y 592 GTTCCCAACCCTTGATAATATCTTGATTATTTTAACTGGCAAAGGTATGCGCACTACATA 651
Db 478 GTAGCCTCCCTACCAACAATCATATCACTCCAGACCTCTTTTGAGGCGACGTCTGAATGATA 537
0Y 652 GCAAGATGTCCAACCTTATGATGAAGGTGTGATTTGCTGGGAGCCTTATGTGCAAGCACATGCT 711
Db 538 GCAAAGGTGTCAACACGTGGGAAGGTGTGCGATTTGGCGGGGTACCAAGGGATGGAAAGCCATGCT 597
0Y 712 GGATATACATCTGTGTGATTTGGCTGCTTTTGATCTCTGCTTAATATGACGACACAAAAGTTGAC 771
Db 598 GGCTATACCTCTGTGTGGCTGGCCGCCCTGTGTAATCTCTCAAGAGGAACGTTCTCTGAC 657
0Y 772 TTCCCTGATTTGATTTGGCTGGGTGGCTTTTTCGTCA--ACGAGTGAATGCGGATTTCAA 828
Db 658 TTGACAGCTTTATTCAAATGGGTGACAAAGCGGCACATGCTATTGGAAGAGGATTTGAC 717
0Y 829 GCGAACAACTAATAATTTGATTTGGTGTGTTGCTGACGCTTTTGCGAG 874
Db 718 GCGCGCTGCACACAGCTGTGTGATGTGCTGCTACTCTTGCGCAG 763

RESULT 10
PCT-US93-08062-B
Sequence 8, Application PC/TUS9308062
GENERAL INFORMATION:
APPLICANT:
SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.
SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.
SEQUENCE CHARACTERISTICS: REISS, YUVAL.
SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.
ADDRESSEE: METHODS AND COMPOSITIONS FOR ADDRESSING THE IDENTIFICATION, ADDRESSING: CHARACTERIZATION AND ADDRESSER: INHIBITION OF ADDRESSER: FARNESYLTRANSFERASE NUMBER OF SEQUENCES: 71 CORRESPONDENCE ADDRESS: ADDRESSEE: ARNOLD, WHITE & DUKKE STREET: P.O. BOX 4433 CITY: HOUSTON STATE: TEXAS COUNTRY: UNITED STATES OF AMERICA ZIP: 77210 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK/ASKII COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/08062 FILING DATE: AUGUST 24, 1993 CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/935,087 FILING DATE: 24 AUGUST 1992 (24.08.92) NAME: UNKNOWN ATTORNEY/AGENT INFORMATION: NAME: PARKER, DAVID L. REGISTRATION NUMBER: 32,165 REFERENCE/DOCKET NUMBER: UTPJ377PCT TELECOMMUNICATION INFORMATION: TELEPHONE: 512-320-7200 TELEFAX: 512-474-7577 TELEX: NOT APPLICABLE INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 1248 nucleic acids

```

```

: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: Linear
PCT-US93-08062-8

Query Match      14.7% ; Score 200.4 ; DB 5 ; Length 1248 ;
Best Local Similarity 56.2% ; Pred. No. 6,46-52 ;
Matches 397 ; Conservative 0 ; Mismatches 306 ; Indels 3 ; Gaps 1,

OY 172 ATGTGAGAGTGGGGGTGATCAGCATATCGATTCGTGACGGCCCTGGGCGTAGACATATG 231
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 58 AGCGTCTGTTTGGAGAGGGAGAACACTTCATTTATCTGAAABAAGGCCCTTGCACAACTG 117

OY 232 GGACCACCCCTTCATGTTCTAGATGCCAATGCCCTTGGCTATCTACTGATGGTTCAT 291
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 118 ACAATATCCCTATAGTGTCTGATGTGCACCCGCCCATGCGCTCTTATGGATCTGCAC 177

OY 292 CCACTTCTTGTGTGATGAGACACTTGATGTATCTTGTGAATGATATCATAGACTTC 351
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 178 AGCTTGAACCTGTAGATAGACCATCCGCCAGATAGTGGCTACAGATGTGTCTAGTTC 237

OY 352 TTAGCTGATGTGAGATAAAGTGTGATATATGTTGTGACTGTGACACAGTTGCTTAC 411
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 238 CTGAGCTGTGTGACAGCCACAGAAAGTGGCTTTGGAGAGGACCCGGTCAAGTATCCACAC 297

OY 412 CTACCTACGACTTATCTCTGTAAATACACTTGGACATATAGGAGACGAGAAAGACTTG 471
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 298 CTTCACCCACATATGACAGAGTCAATGATGTCTCATTCATTTGGCCACCGAGGCCAT 357

OY 472 TCATCATCATTAAGGGCAACCTGTACATTTTATGTCGACAGATGAAGAATGTACAGT 531
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 GACATCTATTACAGAGAGAGCTTCTTCAGTATTTTGTACTCCCTTAAAGCAACCTGACGG 417

OY 532 GCTTTCGAAATGCATGATGSGTGGCGCAATTTGTCGCTGCTCTACACCGCTATATACG 591
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 418 TCCTTCTCATGATGATCGGAGGTGAGTGTGATGTGACAAACGCACTGTGCGCTCC 477

OY 592 GTTCCGACGCTTGTGAATATCTGCAATTTTAACTGGCAAAAGCTGTAAGCGCACTACAT 651
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 478 GTACCCCTGCTGACCAACATCATCACTCCACACCTCTTTGAGGGCACTGCTGAATGGAT 537

OY 652 GCAAGATGTCAAACTTATGAAAGTGTATTTGCTGGGAGACCTTATGCTGAAGCAACTGT 711
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 538 GCAAGGTGTCAAACTGTGGAAGGTGCATTTGCGGGATCCAGCAGGATGTAAGGCCATGT 597

OY 712 GGGTATCATCTGTGTGATTTGCTGTTTGAATCTGCTTATATGAAGGCAAGAAAGTTTG 771
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 598 GGGTATCATCTGTGTGATTTGCTGTTTGAATCTGCTTATATGAAGGCAAGAAAGTTTG 657

OY 772 TTGCGTATTTGAATGGCTGGGTGGCTTTTCTCA--AGGAGTGAATCGGATTTCA 828
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 658 TTGAAGAGCTTATATCAATATGGGTGACAAACCGGAGATGTATTTGAAGAGGATTTCA 717

OY 829 GGACGAACTAATAATTTGTTGATGGTTGTCTCTCTTTTGGCAGG 874
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 718 GGCGGCTGCACAAGCTGGTGGATGGCTACTCTCTTGGCAGG 763

RESULT 11
US-08-424-268-5
: Sequence 5, Application US/08424268
: Patent No. 5821118
: GENERAL INFORMATION:
: APPLICANT: Omer, Charles A
: APPLICANT: Diehl, Ronald E
: APPLICANT: Glibbs, Jackson B
: APPLICANT: Kohl, Nancy E
: TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
: TITLE OF INVENTION: Transferase
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merck & Co., Inc.
: STREET: P.O.Box 2000

```



```

: TITLE OF INVENTION: Transferrase
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merck & Co., Inc.
: STREET: P.O. Box 2000
: CITY: Rahway
: STATE: New Jersey
: COUNTRY: United States of America
: ZIP: 07065-0907
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/10442
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/968,782
: FILING DATE: 10/30/92
: ATTORNEY/AGENT INFORMATION:
: NAME: Mulhaid, David A
: REGISTRATION NUMBER: 35,297
: REFERENCE/DOCKET NUMBER: 18858
: TELECOMMUNICATION INFORMATION:
: TELEFAX: (908) 594-4720
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2546 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: PCT-US93-10442-19

Query Match
Best Local Similarity 14.58; Score 197.2; DB 5; Length 2546;
Matches 395; Conservative 0; Mismatches 308; Indels 3; Gaps 1;

172 ATGCTAGAGCTGTGGCTGATCAAGATATGAGTATGACCTGGGCTGAGCATATG 231
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 230 AGGCTTTGTTGACAGAGGAGAAAGCACTTCATTATCTGMAAAGCCCTTGACACTG 289
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 233 GGACAGCCTTTCATGTTCTAGATGCCAATCGCCCTTGCTATGCTACTGATGTTTAT 291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 290 ACAGATGCTATGATGTCTGATCGAGCGCCCAATGCTCTCTATTGGATCCCTGAC 349
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 292 CCACCTGCTTGTGATGATGAAGCACTGATGATGATGATGATGATGATGATGATG 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 350 AGCTTGAACGTAGATGAACCATCCCAATGATGATGATGATGATGATGATGATG 409
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 352 TTAGTGCATGTCAGATGAAGATGATGATGATGATGATGATGATGATGATGATG 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 410 CTGGAGCTGTCTGAGAGCCCAAGAGGCTTTGGAGGAGGACCGGTCAGTATCAAC 469
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 412 CTAGTACGACTTATGCTGCTGTAATACATTTGATGACATATGAGAGGCAAGACAT 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 470 CTTCAGCCCATATGACAGGAGCAATGATGATGATGATGATGATGATGATGATG 529
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 472 TCATCAATCATAGGAGCAACCTGTACATTTTATGCTGACATGAAAGATGTATCAG 531
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 530 GACATCATTAACAGAGAGAGCTTCTTCACTATTTTACTCCCTGAAGCAACCTGAG 589
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 532 GCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 590 TCCCTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 649
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 592 GTTGGACACCTTGTGATATTTCTGATTTTAACTGCAAAAAGGTGTAGGACATGAT 651
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 650 GTAGCTCTGTCAGCAACATCATCATCATCATCATCATCATCATCATCATCATCAT 709
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```

Qy 652 GCAAGTGTCAAACTATGAAAGTGTATGTTGCTGGGAGCCTTATCTGAAGCAATG 711
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 710 GCMAAGTGTCAAACTGAGAGGATGAGGATGAGGAGGATGAGGATGAGGATGAGG 769
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 712 GGGTATACATTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 771
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 770 GGCTATACCTTCTGTGAGGCTGAGGCGCTGATATCTCAAGAGGAACTTCTTGA 829
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 772 TTGCCTACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 828
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 830 TTGAAGACCTTATTAACATGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 889
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 829 GGACGACCTAATTAATTTGATGATGATGATGATGATGATGATGATGATGATG 874
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 890 GGCCGCTCAACAAAGCTGTGATGATGATGATGATGATGATGATGATGATGATG 935
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-09-387-574-3
: Sequence 3, Application US/09387574
: Patent No. 6168951
: GENERAL INFORMATION:
: APPLICANT: Cahoon, Rebecca E.
: APPLICANT: Kinney, Tony
: APPLICANT: Rafalski, Antoni
: TITLE OF INVENTION: Plant Geranylgeranyl Transferases
: FILE REFERENCE: BB-1239
: CURRENT APPLICATION NUMBER: US/09/387,574
: CURRENT FILING DATE: 1999-08-31
: EARLIER APPLICATION NUMBER: 60/098,743
: EARLIER FILING DATE: September 1, 1998
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: Microsoft Office 97
: SEQ ID NO: 3
: LENGTH: 1306
: TYPE: DNA
: ORGANISM: Glycine max
: US-09-387-574-3

Query Match
Best Local Similarity 4.38; Score 59; DB 4; Length 1306;
Matches 206; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

478 ATCATAGAGGCAACCTGTACATTTTATGCTGCAGATGAAAGATGATCAGGCTTTC 537
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 409 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 468
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 538 AGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 597
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 469 TCAGGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 598 ACCCTTGAATATTTCTGATTTTAACTGCAAAAAGGTGTAGGAGCACTATGATCA 657
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 529 TCATATTTACATCGCTTGATTAATATGATGATGATGATGATGATGATGATGAT 588
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 658 TGTCAACTTATGAGAGGATGATGATGATGATGATGATGATGATGATGATGATG 717
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 589 TGTCAAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 648
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 718 ACATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 777
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 649 ATTTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 708
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 778 AGTTTGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 837
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 709 CTACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 768
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 838 AATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 897
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 769 GAGAAACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 898 AAGTTAATTAAGATTTGATTAAGCAATTGA 928
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db 829 AGGTTACATTGGATTAGTAGAGAGAGCTTA 859

Search completed: November 1, 2002, 15:40:38
Job time : 60 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OK nucleic - nucleic search, using sw model

Run on: November 1, 2002, 12:41:54 ; Search time 1796 Seconds
(without alignments)
10212.896 Million cell updates/sec

Title: US-09-786-675-11

Perfect score: 1359
Sequence: 1 atgagacccctcccgagtc.....agtctctcagaagatga 1359

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: em_estha:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gD_estl:*
10: gD_estl2:*
11: gD_hic:*
12: gD_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	354	26.0	794	10	BG594738
2	328.6	24.2	675	9	AL506683
3	309.2	22.8	715	9	BE214204
4	306	22.5	694	10	BF634888
5	295	21.7	731	10	BG600901
6	275.4	20.3	582	9	BE194182
7	254	18.7	639	9	AL509620
8	248	18.2	639	10	BG095687
9	242	17.8	521	9	BE129712
10	232	17.1	533	9	AW120078
11	225.8	16.6	506	10	BM177970
12	215.6	15.9	488	10	BF097538
13	211.8	15.6	457	9	AT488509
14	202	14.9	2707	11	BC013574
15	188	13.8	553	9	AW508684
16	182.8	13.5	579	9	BE022297
17	179.6	13.2	541	9	AL510109

18	160.6	11.8	796	9	AU135633	AU135633
19	159.8	11.8	671	9	AL586940	AL586940
20	156.8	11.5	937	10	BG25222	BG25222
21	155.2	11.4	417	10	BM172851	BM172851
22	154.2	11.3	841	10	BG761213	BG761213
23	144.8	10.7	600	10	BG801722	BG801722
24	143.6	10.6	636	9	AL638378	AL638378
25	143	10.5	771	10	BF162476	BF162476
26	142.6	10.5	778	9	AT151779	AT151779
27	142	10.4	511	10	BJ187628	BJ187628
28	138.2	10.2	469	9	AW56366	AW56366
29	137.6	10.1	690	10	BJ335119	BJ335119
30	136.2	10.0	856	10	BJ246235	BJ246235
31	134.2	9.9	1804	10	BG257205	BG257205
32	132.2	9.7	748	10	BJ520188	BJ520188
33	132.2	9.7	759	10	BJ550578	BJ550578
34	131	9.6	429	10	BJ424834	BJ424834
35	131	9.6	589	10	BE824252	BE824252
36	129.2	9.5	632	10	BM488977	BM488977
37	128	9.4	774	10	BE398203	BE398203
38	122.2	8.9	225	9	AW683980	AW683980
39	121.2	8.8	623	10	BJ111625	BJ111625
40	119.2	8.8	741	10	BG128793	BG128793
41	118.8	8.7	1004	10	BG761267	BG761267
42	118.8	8.7	1004	10	BM407893	BM407893
43	118.4	8.7	697	10	BJ178887	BJ178887
44	117.8	8.7	710	10	BJ178887	BJ178887
45	115.8	8.5	598	10	BJ516491	BJ516491

ALIGNMENTS

RESULT 1
LOCUS BG594738 794 bp mRNA linear EST 12-APR-2001
DEFINITION ESR493416 cSTS Solanum tuberosum cDNA clone cSTS66 5' sequence,
mRNA sequence.
ACCESSION BG594738
VERSION BG594738.1 GI:13612878
KEYWORDS EST.
SOURCE Solanum tuberosum
ORGANISM Solanum tuberosum
potato.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 794)
REFERENCE van der Hoeven,R., Bezzerides,J., Sun,R., Cho,J., Chitemingo,A.,
Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
Generations of ESTs from sprouting potato eyes
Unpublished (2000)
JOURNAL
CONTACT Cathy Ronning
The Institute for Genomic Research
For clone info, please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdraatresgen.com
Seq primer: M13F-R.
Location/Qualifiers
1..794
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTS66"
/clone_lib="cSTS"
/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/note="Vector: Bluescript SK(-); Site1: EcoRI; Site2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 20C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."

BASE COUNT 208 a 149 c 206 g 231 t

BASE COUNTRY	ORIGIN	185 a	131 c	167 g	210 t	1 others
/clone_1b="Drought"						
/clone_type="plantlets"						
/dev_stage="Pooled timepoints"						
/note="Vector: lambda zap; Contains a mixture of entire plantlets harvested in a series of days-post-watering timepoints."						

Query Match	22.58;	Score 306;	DB 10;	Length 694;
Best Local Similarity	66.58;	Pred. No. 3.5e-68;		
Matches 438; Conservative	0;	Mismatches 221;	Indels 0;	Gaps 0;

QY	64	GACCTACCGGAGGCTCAGCGGAGCGAGCGAGTGAAGGTGGAGCCAGGGTTGGC	123
Db	36	GAGCACCATTCTCCAAAGGTGAGTCAAGATGATAGTAAAGATCAAAAGTCTTT	95
QY	124	GACATCTACCGCTCCCTTTCCGGGCCCGGCCAACAGAAATCTCATCTGTAGAGCTG	183
Db	96	CACATTTTATCACTCTTTTCTACTATTCTCTTAAAGGCTCAATCCCTCATTTGGAAATGG	155
QY	184	TGCGGTCATCAGATATTCGATGTCTGACGCGCTGGGCTGAGGACATATGGAGCCAGCCCTTT	243
Db	156	CAAGGAGATTAACACATCCAGATATCTCTTTTAAAGGACATCTTCGCCATCTCCGGTACAGCTTTT	215
QY	244	CATCTTTAGATGCATATGCGCCTTGGCTATGCTACTGATGATGTTTCATCCACTGTGCTTTG	303

Db 216 TCAGTATTGATGCAAAATCGACCCGTGGCTGTGTTACTGGATTATTCACGCAATTCGCTTTG 275

Oy 304 CTCGATGAAGCACTTGATGATGATCTTTGAGAAATGATATCATAGACTTTCTAGCTCGATGT 363

DB	216	TTGGGACAAACATATGATGATGACCTTGAAGATTAACACAGTTGATTTTCTTAACCGGTTGC	335
QY	364	CAGCATAAAGATGATGATATAGTGGTGACCTGGACACTTGCCCTCACCTAGCTACGACT	423

424 TATGCTGCTGAATACACTTTGGACAAATAGGGAAGCGAAGAGCATTTGTCATCAATCAAT 483

484 ACGGCGAAGCTGTACAAATTTTATTCCTCAGATGAAGAATGTATCAGTGTCTTTCAGAATG 543
 11 11 1111 11111111 11111111 11111111 11111111 11111111 11111111
 456 AGAGATAAATTGTATGGGCTTATATCCGCGGATATATACATGCGGATATATGCGGATATATGCGGATATG 515
 11 11 1111 11111111 11111111 11111111 11111111 11111111 11111111 11111111

[illegible]

Oy 604 GCGATATTCTTCATTTTAAACGCGCAAAAGGTGAGCGCACCATAGCCACAAGTGTCAA 663
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 576 CTAAACATTTTGCATGATGAGCGCATCAAGAAGTTGGAGACTTCATATTAAAGTGTCAA 635

QY 664 ACCTATGAAAGGTGGTATTGCTGGGAGACCTTAGTGCTGAAGCACATGGTGGTATACATTT 722
 || ||||| ||||| ||||| ||||| | ||||| ||||| |||||
Db 636 ACATATGAGGGGTGCATTGCTGCTGGTAGCCCTGTTTCTGANGCTCATGGGGGGTATACCTTT 694

RESULT 5				
BG600901				
LOCUS	BG600901	731 bp	mRNA	linear
				EST 12-APR-2001

miRNA sequence,
ACCESSION BG600901
VERSION BG600901.1 GI:13618025

SOURCE	ORGANISM
potato,	<i>Solanum tuberosum</i>
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots.

REFERENCE
1 (bases 1 to 731)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chlemingo, A.,
Mazurkiewicz, J., and Kozminski, A., 1990, *Journal of Virology*, 64, 1000-1005.

TITLE Gougeon, O., Bell, C. R., Romling, C., Tanksley, S. and Baker, B.
JOURNAL generations of ESTs from sprouting potato eyes
COMMENT Unpublished (2000)
Contact: Cathy Romling
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F.R.

```

source
1. .731
/organism="Solanum tuberosum"
/cultivar="Kennebec"

```

```

/clone="csts30g24"
/clone.lib="csts"
/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/notes="Vector: pbluescript SK(-); Site: 1. EcoRI; 5'
XhoI; Various sizes of sprouting eyes (2mm to 15mm)
taken from tubers. The tubers were incubated at 25°C
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal
tubers."

```

Query Match	21.7%	Score 295;	DB 10;	Length 731;
Best Local Similarity	66.88;	Pred. No. 2.5e-65;		
Matches 435;	Conservative	0;	Mismatches 215;	Indels 1;

Oy 72 GAGCGTCACGCGTGACCGCAGGTGAGCAGATGAAAGTGGAGGCCAGGGCTTTGGCGCATCTA
||| ||||| | |||
Db 82 GAACGTGACGAGAACCGCTGGAGATCAATGGGTGGTGGAGCGCTGGAGTCCGAGAGATATA

142 CGATTATTTCACAGCATTTCCCAATTCCCTGTCGACCTCATAGAGCTGGAACGTGA

202 CAACACTTCGATATTCTTAGCCAAAGGTCTCAGAAACTGTGTCGCTTTTCCGTTTT

Db 262 GGATGCCAGTCGACCACCATGGCTTTGCTACTCGATACCTTCATTCGAATTGCTTTGTGGGACA

Db	322	ATCTATTGATGCCAAACCTGGAAATGATGCGACTGACTTTCTGACCCCGTTGCCAGGATAA
Qy	372	AGATCGTGATATAGTGTGCTGGACCTGGACAGTGTGCTCACCCTAGCTAGCACTTATGCTGC

Db 382 AGATGGTGGCTATGGAGCTGGACCTGGTCTAGATGCCATCTTGGCACTACTTATGCTCC
Qy 432 TGTAAATACACTTGTGCAATAGGGAGCGCAAGAGCATTTGTATCAATCAATAGGGCAA

492 CCTGTACAATTTATGCTGCACATGAAGATGTATCAGTGCTTTCAGAAATGCATGATCG
|||||

552 TGGCCAAATTGATGTCCTGCTTCTACACGGCTATATGGCTTGGCAGCCTTGCAATAT

612 TCCTGATTTTAACTGCAAAAGGTGTAGCGACATAGCAAGATGTCAACCTATGCA
 622 TCTGATATGACGACCTGATATTCATGCTCTCTGCG - AAATTCATATCTCAAACTCTCTCAGAGATCTATGCA
 632 TCTGATATGACGACCTGATATTCATGCTCTCTGCG - AAATTCATATCTCAAACTCTCTCAGAGATCTATGCA

672 AGGTCGTATTCCTGGGAGCCCTATGCTGAGACACATGGTGGCTATACATT 722

Db 681 AGGTGAATTGCTGCGACCAAGTTCTGAGCTCATGGTGGTACTTT 731

RESULT 6
LOCUS BE194182
DEFINITION BE194182 582 bp mRNA linear EST 22-OCT-2001
HVSMEH0084H13f Hordeum vulgare 5-45 DAP spike EST library
HVCDA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH0084H13f,
mRNA sequence.
BE194182
VERSION BE194182.1 GI:8706368
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
1 (bases 1 to 582)
Ming, R., Close, T.J., Kleinholz, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Close, S.J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex 5-45 DAP spike cDNA library
Unpublished (2001)
Contact: Ming RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 161
Seq primer: AATTACCTCCTCACTAAGCG
High quality sequence start: 12
High quality sequence stop: 527.
Location/Qualifiers
1..582
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEH0084H13f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVCDA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP, Site_1: EcoRI, Site_2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,
30 and 45 DAP (Fenton). Total RNA was prepared from each
pool, equal quantities of all six RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary,
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give plasmid SK(-) cDNA phagemids
(Choi) in the TJ Close lab at the University of California,
Riverside. Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Ming). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI.
(Ming, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Ming R, Kleinholz A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30
(http://wheat.pw.usda.gov/ggpages/bgr/31/cover.html)."

BASE COUNT 123 a 168 c 176 g 114 t 1 others

ORIGIN

Query Match 20.3%; Score 275.4; DB 9; Length 582;
Best Local Similarity 75.9%; Pred. No. 2,5e-60;
Matches 366; Conservative 0; Mismatches 112; Indels 4; Gaps 2;

13 CCGCAGTGGAGCGCCGACGAGACGACCGGCGGCGGATCCGACTACCG 72
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 102 CCGCAGCGCCCTCCCGCGGGGAGACCGCTCGAGAGCAATCGGCCGCGGAGTGGCC 161
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Qy 73 AGCGTCACGTCAGCAGAGTCGAGACAGATGAGGTGAGGCCAGGTTGGCAGATCTAC 132
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 162 GCGTCACCGTCGAGCGAGTCGAGACAGATGAGGTGAGGCCAGGTTGGCAGATCTAC 221
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Qy 133 CCGCTCTCTTGGGGCCGCCACACAGCAATTCATCTAGCTGGCGTAT 192
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 222 CCGGCTCTTTCGAGCGCGCCGACGCAAGTCGCGCGTGGAGCTGGGGCGAT 281
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Qy 193 CAGCATTCGAGTATCTGACGCTCGGCTGAGCATATGAGACGACCTTTGATCTGTA 252
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 282 CAGCATTCGAGTATTCAGCAAGGCTGAGCATCTTGACACTTCATCTGCTGCTC 341
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Qy 253 GATGCCAATCGCCCTGGCTATGCTACTGATGATGATTCACCTTCTTGGATGAA 312
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 342 GATGCCAACCACCTGGTATGCTATGATGATGATGATGATGATGATGATGATGATG 401
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Qy 313 GCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 402 AGCTTGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 461
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Qy 373 GATGCTGATATAGTGTGACCTGACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 462 CATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 520
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Qy 433 GTAAATACAC--TTTGACAAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 489
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 521 GTAAATACACATTTTACCATATGAGAGTGAAAAAGACATATCATCATTTATAAGGA 580
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Qy 490 AA 491
||
Db 581 AA 582

RESULT 7
LOCUS AL509620/c 639 bp mRNA linear EST 04-JAN-2001
DEFINITION AL509620 Hordeum vulgare Barke developing caryopsis (3--15 DAP)
AL509620
ACCESSION AL509620
VERSION AL509620.1 GI:12036123
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
1 (bases 1 to 639)
Michael, M., Weschke, M., Pleissner, K., P. and Graner, A.
EST sequencing and analysis in barley
Unpublished (2000)
Contact: Michael M
Institute for Plant Genetics and Crop Plant Research
Corrensstr.3, D-06466 Gatersleben, Germany
Email: michael@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: M3uni primer for 3' end.
Location/Qualifiers
1..639
/organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
/clone="HY02G01u"
/clone_lib="Hordeum vulgare Barke developing caryopsis
(3..15.DAP)"
/tissue_type="developing caryopsis (3..15.DAP)"
/lab_host="XLOLR"

FEATURES
source

JOURNAL COMMENT

University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946003 row: D column: 09.

FEATURES SOURCE

Location/Qualifiers

1. 521
/organism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_id="946 - tassels primordium prepared by Schmidt lab"

/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to inflorescence development"
/lab_host="X10LR"

/note="Organ: tassels; Vector: HybridZAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."

BASE COUNT 151 a 118 c 97 g 155 t

ORIGIN

Query Match 17.8%; Score 242; DB 9; Length 521;

Best Local Similarity 100.0%; Pred. No. 1e-51;

Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1118 CTCAGTACTAGAGGAGCGCTTGAGGATTAAGCTGGAAGACAGAGATCACTATCATTT 1177

Db 371 CTCAGTACTAGAGGAGCGCTTGAGGATTAAGCTGGAAGACAGAGATCACTATCATTT 312

QY 1178 CATGCTACTGCTCAGTGGCTCGCAGTTAGCCAGTACAGTGCATGATGATCTGCTT 1237

Db 311 CATGCTACTGCTCAGTGGCTCGCAGTTAGCCAGTACAGTGCATGATGATGCTT 252

QY 1238 CGTGCCATTACCTAGCATGTGCTGGACCGTACTTAATTTGCTGAGCCATCCATC 1297

Db 251 CGTGCCATTACCTAGCATGTGCTGGACCGTACTTAATTTGCTGAGCCATCCATC 192

QY 1298 CACTCTACAATCTGTCTCTAGATTAAGTACATACAGCTATGATCTCTCAGAAAGT 1357

Db 191 CACTCTACAATCTGTCTCTAGATTAAGTACATACAGCTATGATCTCTCAGAAAGT 132

QY 1358 GA 1359

Db 131 GA 130

RESULT 10

AM120078 533 bp mRNA linear EST 22-OCT-1999

LOCUS 614083B05.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA,

DEFINITION mRNA sequence.

ACCESSION AM120078

VERSION AM120078.1 GI:6095411

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoidae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 533)

AUTHORS Walbot, V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 614083 row: B column: 05.

FEATURES SOURCE

Location/Qualifiers

1. 533
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_id="614 - root cDNA library from Walbot Lab"

/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="X10LR"
/note="Organ: root; Vector: pBluescriptII SK⁺; Site_1: EcoRI; Site_2: XhoI; 3-4 days old root tissue from Walbot Lab (LM)"

BASE COUNT 157 a 109 c 103 g 162 t 2 others

ORIGIN

Query Match 17.1%; Score 232; DB 9; Length 533;

Best Local Similarity 100.0%; Pred. No. 4e-49;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1118 CTCAGTACTAGAGGAGCGCTTGAGGATTAAGCTGGAAGACAGAGATCACTATCATTT 1177

Db 302 CTCAGTACTAGAGGAGCGCTTGAGGATTAAGCTGGAAGACAGAGATCACTATCATTT 361

QY 1178 CATGCTACTGCTCAGTGGCTCGCAGTTAGCCAGTACAGTGCATGATGATCTGCTT 1237

Db 362 CATGCTACTGCTCAGTGGCTCGCAGTTAGCCAGTACAGTGCATGATGATCTGCTT 421

QY 1238 CGTGCCATTACCTAGCATGTGCTGGACCGTACTTAATTTGCTGAGCCATCCATC 1297

Db 422 CGTGCCATTACCTAGCATGTGCTGGACCGTACTTAATTTGCTGAGCCATCCATC 481

QY 1298 CACTCTACAATCTGTCTCTAGATTAAGTACATACAGCTATGATCTCTCAGAAAGT 1349

Db 482 CACTCTACAATCTGTCTCTAGATTAAGTACATACAGCTATGATCTCTCAGAAAGT 533

RESULT 11

BM177970 506 bp mRNA linear EST 06-DEC-2001

LOCUS saj67e09.y1 Gm-c1072 glycine max cDNA clone SOYBEAN CLONE ID:

DEFINITION Gm-c1072-4818 5' similar to SW:PF0B_P04903 PROTEIN

FARNESYLTRANSFERASE BETA SUBUNIT ; mRNA sequence.

ACCESSION BM177970

VERSION BM177970.1 GI:17401188

KEYWORDS EST.

SOURCE soybean.

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

REFERENCE 1 (bases 1 to 506)

AUTHORS Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corvett, V., Khanna,

A., Holla, B., Maitra, M., Hillier, L., Kuecha, T., Martin, J., Beck, C.,

Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers,

J., Peterson, B., Waller, T., Gibbons, M., Pape, D., Harvey, N., Schurk,

R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann,

R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Oy 252 AGATGGCAATGCCCTTGGTGCATTCGTACTAGATGGTATGCATCACTTCTTGGTCATATA 311
 Db 191 GGATGCCAGTGCACCTATGGCTTTGGTACTGGGACACTTATTCATTCATCGCTTTGGTGAC 250
 Oy 312 AGCACTGATGATGATCTTGAGATATATCATATGACTCTTACTCTGATGTCAGATATA 371
 Db 251 ATCTATTTGGTGGCAAACTGGAAAAATGATGCAATTTGACTTTCTGACCCGTTGGCAGATATA 310
 Oy 372 AGATGGGATATAGTGGTGGACCTGGACAGTGGCTCACTACTCTGCACTATATCTGC 431
 Db 311 AGATGGGCGTATAGGAGGTGGACCTGGTGCACATGCTCATCTTGGCAACTCTATTATGCTGC 370
 Oy 432 TGTAAATACCTTGTGCACAAATAGGAGCGAAAGACATTTGCATCAATCAATAGGGCAA 491
 Db 371 AGTCATATCTCTAATTAACCTTTGGGCAAACTGAAAGCTCTGTGATCAATTAATAGAGAAA 430
 Oy 492 CCTGTCAATTTTATCTCGACATGAAGAATGTATATCAAGTGCCTTTTCAGAAATGCATAT 549
 Db 431 GTTGTGACACTTTTCTCTCGAATGAAGAAGCAGTGGTGATTCAGGATGACAT 488

RESULT 13	LOCUS	DEFINITION	LOCUS	DEFINITION
AI488509	AI488509	tomato ovary, TMU Lycopersicon esculentum cDNA clone	457 bp mRNA	linear EST 18-MAY-2001
ACCESSION	AI488509	tomato ovary, TMU Lycopersicon esculentum cDNA clone	457 bp mRNA	linear EST 18-MAY-2001
VERSION	AI488509.1	tomato ovary, TMU Lycopersicon esculentum cDNA clone	457 bp mRNA	linear EST 18-MAY-2001
KEYWORDS	GI:4383880	tomato ovary, TMU Lycopersicon esculentum cDNA clone	457 bp mRNA	linear EST 18-MAY-2001
SOURCE	tomato.	tomato ovary, TMU Lycopersicon esculentum cDNA clone	457 bp mRNA	linear EST 18-MAY-2001

REFERENCE
1 (bases 1 to 457)
Alcala, J., Vrabalov, J., White, R., Matern, A. L., Vlsion, T., Holt, I. E.,
Liang, F., Upton, J., Ronning, C. M., Craven, M. B., Fujii, C. Y., Bowman,
C. L., Nieman, W., Fraser, C. M., Venter, J. C., Martin, G. B., Tanksey,
S. D. and Giovannoni, J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
Contact: CUGI

100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.
Location/Qualifiers
1..457

```

/cclone.lib="tomato ovary, TAMO"
/tissue.type="carpel"
/dew_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XLI Blue MRF"
/node=Vector: pBluescript SK(-); Site-1: EcoRI; Site-2:
XhoI; cLED - Tomato Carpel EST Library. OligoDT primed and
directionally cloned cDNA in vector lambda ZAP II with 5'
and 3' ends located at the EcoRI and XhoI sites,
respectively."

```

Query Match	15.6%	Score 211.8	DB 9	Length 457
Best Local Similarity	66.6%	Pred. No. 6e-44		
Matches 307	Conservative 0	Mismatches 152	Indels 0	Gaps 0
OY	100	ATGAGGTGGAGGCCAGGTTGGCGACATCTACGCCTCCCTTCCTGGGGCCGCCCCAAC	159	
Db	3	ACGAGGGTGGAGCGTGCGATCCGAGAGNATACGATTATTTCTCAGACATTTTCCCCAAC	62	

Oy	160	ACAAATCCATCATGTAGAGCGTGGCGGTATGACGATATGAGTATCTGAGACCGTGG	219
Oy	161	TTCTCCGCTCCCACTCATAGAGATCGAACGTGACAAACCTTCGGTATTCTTAAGCCAAGGT	212
Oy	220	CTCAGCCATATGGGACCGACCTTTTCATGTTTCTAGATGCCAATGGCCCTTGGCTATGCTAC	279
Oy	123	CTCGAAAACTTGGTGGCGCGTTTTTTCGGTTTGGATGGCACTCCACCATGGCTTTGCTAC	182
Oy	280	TGCATGGTTCATCCACTTCTTGGCTGATGAGACACTTGATGATGATCTTGGAAATGAT	339
Oy	183	TGGACATTCATTCATTCATCGCTTGTGGGAGAACTTATTTGGTGGCAAACTGGAAATGAT	242
Oy	340	ATCATACATCTTCTACCTGATGTGAGATTAAGATGGTGGATTTACTGGTGGACCTGGA	399
Oy	243	GCATATACATTTTGCAGCCGTGGCCAGGATTAAGATGGTGGCTATGAGAGGTGACCTGGT	302
Oy	400	CAGTTGGCTCACCTAGCTACGACTTATGCTGCTGTAAATACACTTGTGACAAATAGGAGC	459
Oy	303	CAGATGGCTATCTTGCACACTACTTATGCTGACGACCAATTCACATAATACCTTTGGGCAAA	362
Oy	460	GAAGAGCATTTGATCAATCAATACATAGGAGCAACCTGTAATTTTATGCGAGATGAAA	519
Oy	363	CTGAACTCTGTCATCATTAATTAAGAAAAAGTTGTACACATTTTGTGCTGCCAATGAAA	422
Oy	520	GATGTATCAGGTGCTTTCAGAAATGCATGATGGTGG	554
Oy	423	GACCGAAGTGTGATTCAGAGACCGATGGTGG	457

RESULT	14
LOCUS	BC013574
DEFINITION	BC013574 2707 bp mRNA linear HTC 07-SEP-2001 Homo sapiens, farnesyltransferase, CAAX box, beta, clone
ACCESSION	IMAGE:3898137, mRNA. BC013574
VERSION	BC013574.1 GI:15488887
KEYWORDS	HTC.
SOURCE	human, human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 2707)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGCC) Cancer Genomics Office, National Cancer

REMARK	COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov	
Contact: MGC help desk	
Email: cgabs-rt@mail.nih.gov	
Tissue Procurement: ATCC	
cDNA Library Preparation: Life Technologies, Inc.	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305	
Web site: http://www.shgc.stanford.edu	
Contact: (Dickson, Mark) mcdeparill@stanford.edu	
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.	

Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRM Plate: 14 Row: k Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA q1: 292032
This clone has the following problem: Incomplete processing.

```

FEATURES
source
location/Qualifiers
1. 2707
/organism="Homo sapiens"
/db_xref="LocusID:2342"
/db_xref="taxon:9606"

```

```

/clone="IMAGE:3898137"
/tissue_type="Pancreas, epithelioid carcinoma"
/clone_id="NH_MCC_70"
/lab_host="DH10B"
/notes="Vector: PCMV-SPOBIC"
BASE COUNT      628 a      743 c      692 g      644 t
ORIGIN
Query Match      14.9% Score 202; DB 11; Length 2707;
Best Local Similarity 56.4% Pred. No. 5, 2e-41;
Matches 398; Conservative 0; Mismatches 305; Indels 3; Gaps 1;

172 ATGCTAGACCTGCGCGATGACATATGATGACGCGCTGAGCATATG 231
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
246 AGCGCTGTTTGCAAGAGGAGACACCTCCATTATCTGAAAGAGCCCTGACACATG 305
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
232 GGACGACCTTTCATGTTGATGACCAATGCGCTGCTATGCTACTGATGATGCTTAT 291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
306 ACAGATGCTTATGATGCTGATGACGCGCCGACGATGCTGCTATGATGCTGCTGAC 365
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
292 CCACCTGCTTCTGCTGATGAGACACTGATGATGATGATGATGATGATGATGATGATG 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
366 ACCTTGGAACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 425
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
352 TTACGTCATGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
426 CTGAGAGCTGTGTCAGAGCCGACAGAGCTGCTTGGAGAGAGACCGGCTGATGATGAC 485
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
412 CTAGCTAGACCTTATGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
486 CTTGACACCCACATGACGACGATGATGATGATGATGATGATGATGATGATGATGATG 545
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
472 TCATCATCATATAGAGGAGACCTGATGATGATGATGATGATGATGATGATGATGATGAT 531
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
546 GACATCATTTAAGAGAGAGAGACCTTCTGATGATGATGATGATGATGATGATGATGATG 605
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
532 GCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
606 TCTTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 665
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
592 GTTGCCAGCTTGTGATATATTTCTGATTTTAACTGGCAAAAGGTAGGCGACATGATA 651
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
666 GTAGCTCTGCTGACCAACATCATCATGACAGACCTTGTGAGGGGACTCTGCAATGATA 725
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
652 GCAAGATGCAAACTTATGAGAGTGTGATGCTGGGAGGCTTATGCTGAACACATGAT 711
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
726 GCAAGTGTGCAAACTTATGAGAGTGTGATGCTGGGAGGCTTATGCTGAACACATGAT 785
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
712 GCGTATACATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 771
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
786 GCGTATACATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 845
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
772 TTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 828
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
846 TTGAGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 905
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
829 GAGAGCACTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 874
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
906 GCGCTGCTGCAACAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 951
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
AM508684      553 bp      mRNA      linear      EST 03-DEC-2001
LOCUS      513508.91 Gm-r1030 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION      Gm-r1030-876 5' similar to SW:PTB_PEA Q04903 PROTEIN
FAIRVIEW/TRANSFERRASE BETA SUBUNIT ; mRNA sequence.
ACCESSION      AM508684
VERSION      AM508684.1 GI:7146762
KEYWORDS      EST.
SOURCE      soybean.
ORGANISM      Glycine max
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

```

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 553)
AUTHORS      Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
               A., Holla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
               Wylie,T., Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers,
               Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuck
               R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., Mcann
               R., Waterston,R. and Wilson,R.
               Public Soybean EST Project
               Unpublished (1999)
               Contact: Shoemaker R/Public Soybean EST Project
               Public Soybean EST Project
               Washington University School of Medicine
               444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: estelaton@wustl.edu
               This clone is available through: Resgen, Invitrogen Corp. 2130
               South Memorial Parkway Huntsville, AL 35801 for further information
               call: (800)-533-4363 or contact via email: cdu@resgen.com
               Insert Length: 1739 Std Error: 0.00
               High quality sequence stop: 430.
               Location/Qualifiers
                   1..553
                       /organism="Glycine max"
                       /db_xref="taxon:3847"
                       /clone="GENOME SYSTEMS CLONE ID: Gm-r1030-876"
                       /clone_id="Gm-r1030"
                       /lab_host="DH10B"
                       /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
               cDNA library was constructed from mRNA isolated from
               immature cotyledons of greenhouse grown plants
               (individual seed fresh weight of 100-300mg). The library
               was prepared using the life technologies psupertscript cDNA
               library construction kit. Complementary DNA was
               synthesized from mRNA using a poly(dT) sequence with a
               NotI restriction site. SalI linkers adapters were ligated
               to the blunt-ended cDNA fragments followed by NotI
               digestion. The cDNA fragments were directionally cloned
               into the NotI-SalI restriction site of the pSPORT1
               vector. The ligated cDNA fragments were transformed into
               E. coli Electromax DH10B host cells. This library was
               constructed by Dr. Lila Vodkin and Dr. Anu Khanna. Note
               that Gm-r1030 is a re-track of Gm-cl007."
BASE COUNT      131 a      139 c      141 g      142 t
ORIGIN
Query Match      13.8% Score 188; DB 9; Length 553;
Best Local Similarity 63.2% Pred. No. 9, 4e-38;
Matches 306; Conservative 0; Mismatches 175; Indels 3; Gaps 1;

70 CCGAGCTCAGCGTGGACGAGTGGACATATAGCTGAGGCCAGGTTGGCACATC 129
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
70 CCGTCTCGGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 129
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
130 TACCGCTCCCTCTTGGGGGCGCGCCACACGAAATTCATGATGATGATGATGATGATG 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
130 TACCAATCTTTCGACCATTCCTCGCAACGCCCAAAACCTCATGTTGAGAGCTCAAGCG 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
190 GATCAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 249
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
190 GATTAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 249
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
250 CTAGATGCAATGCGCCCTTGGCTATGCTAGTATGATGATGATGATGATGATGATGATGATG 309
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
250 TTGAGAGCTAATGACCCCTGCTGCTAGTATGATGATGATGATGATGATGATGATGATG 309
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
310 GAAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
310 GATTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

QY 370 AAAGATGATGATATAGTGGGACCTGGACAGTTGCCACCTAGTACGACTTATGCT 429
    |||||
DB 370 CCGAATGATGATATAGCGGGGACCGACAGATGCTCATATGCGCACAACTTATGCT 429
    |||||
QY 430 GCTTAATACCTGTGACATAGGAGCGAAAGCATTTGTCAATCAATAGC--- 486
    |||||
DB 430 GCTTAATACCTGTGACATAGGAGCGAAAGCATTTGTCAATCAATAGGAGTGA 489
    |||||
QY 487 GGCACCTGTACAAATTTATGCTGCAGATGAAGATGTATCAGTGTCTTCAGAAATGAT 546
    |||||
DB 490 GATTAACCTGTATGGGTTTCTGCGCGGATGAAGCAACCAATGTGATTCAGGATGAT 549
    |||||
QY 547 GATG 550
    |||||
DB 550 GATG 553

```

Search completed: November 1, 2002, 14:50:42
 Job time : 1804 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2002, 16:23:35 ; Search time 50 Seconds
(without alignments)
1004.107 Million cell updates/sec

Title: US-09-786-675-12

Perfect score: 2411
Sequence: 1 MDSPQSTRPTGDDPAAAD.....PLYWVLDKHTAEPFSE 452

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802:*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2411	100.0	452	21	AAV70502	Corn farnesyltrans
2	1368	56.7	429	21	AAV70504	Soybean farnesyltr
3	1306	54.2	313	21	AAV70503	Rice farnesyltrans
4	1205.5	50.0	443	21	AAAG10406	Arabidopsis thalia
5	1205.5	50.0	475	21	AAAG10405	Arabidopsis thalia
6	1192	49.4	444	21	AAAG46813	Arabidopsis thalia
7	1192	49.4	476	21	AAAG46812	Arabidopsis thalia
8	1163.5	48.3	405	21	AAAG10407	Arabidopsis thalia
9	1159.5	48.1	404	20	AAW97867	Arabidopsis farnes
10	1150	47.7	406	21	AAAG46814	Arabidopsis thalia
11	944.5	39.2	437	15	AAAS4829	Beta subunit of bo

12	942.5	39.1	437	15	AAAR9740	Farnesyltransferas
13	942.5	39.1	437	16	AAAR77840	Rat farnesyl prote
14	942.5	39.1	437	17	AAAM04428	Beta subunit of hu
15	940.5	39.0	437	15	AAAR54831	Beta subunit of hu
16	935.5	38.8	440	15	AAAR54832	Beta subunit of hu
17	898.5	37.3	387	16	AAAR77842	Human farnesyl pro
18	898.5	37.3	387	17	AAAM04432	Farnesyltransferas
19	896.5	37.2	387	15	AAAR49735	Farnesyltransferas
20	832.5	34.5	419	22	ABBR71923	Arabidopsis thalia
21	763.5	31.7	298	21	AAAG46809	Arabidopsis thalia
22	756.5	31.4	291	21	AAAG46810	Arabidopsis thalia
23	719.5	29.8	282	21	AAAG46811	Arabidopsis thalia
24	443	18.4	141	21	AAV70505	Soybean farnesyltr
25	359	14.9	355	22	AAV97629	Soybean farnesyltr
26	345.5	14.3	321	21	AAAG17685	Arabidopsis thalia
27	343.5	14.2	313	21	AAAG17686	Arabidopsis thalia
28	340.5	14.1	317	21	AAAG11828	Arabidopsis thalia
29	336	13.9	300	21	AAAG11829	Arabidopsis thalia
30	334	13.9	287	21	AAAG11830	Arabidopsis thalia
31	330	13.7	299	21	AAAG17687	Arabidopsis thalia
32	320	13.3	377	16	AAAR76786	Human GGTase-I bet
33	320	13.3	377	17	AAAM04469	Human geranylgeran
34	313	13.0	376	16	AAAM04470	Rat geranylgeranyl
35	313	13.0	377	16	AAAR76785	Rat GGTase-I beta-
36	304.5	12.6	313	22	AAV97627	Soybean geranylger
37	304.5	12.6	347	22	ABBR66834	Drosophila melano
38	291.5	12.1	318	22	AAV97626	Zea Mays geranylge
39	286	11.9	395	22	ABBR59926	Drosophila melano
40	285	11.8	291	22	AAV97628	Wheat geranylgeran
41	189	7.8	364	20	AAI33873	Candida GGTase I
42	101	4.2	550	22	ABBR27904	Novel human diapo
43	97	4.0	253	20	AAV04477	Rhodococcus rhodo
44	96.5	4.0	2703	22	ABBR60266	Drosophila melano
45	93.5	3.9	1379	22	ABBR05716	Novel human diapo

ALIGNMENTS

RESULT 1	
AAV70502	AAV70502 standard; Protein: 452 AA.
ID	AAV70502
AC	AAV70502;
DT	04-JUL-2000 (first entry)
DE	Corn farnesyltransferase beta subunit.
KW	Corn: farnesyltransferase beta subunit; transgenic plant;
KW	drought tolerance; cell growth.
OS	Zea mays.
PN	W0200014207-A2.
XX	16-MAR-2000.
PD	07-SEP-1999; 99WC-US20419.
PF	08-SEP-1998; 98US-0099521.
PR	(DUPO) DU PONT DE NEMOURS & CO E. I.
PA	Cahoon RE, Miao G, Powell W;
XX	WPI: 2000-256964/22.
DR	N-PSDB; AAZ51791.
XX	New isolated polynucleotide encoding farnesyltransferase polypeptide is
PT	useful for producing transgenic plants with an altered level of
PT	farnesyltransferase .
XX	

KW Rice; farnesyltransferase beta subunit; transgenic plant;
KW drought tolerance; cell growth.
XX
XX Oryza sativa.
XX MO200014207-A2.
XX
PD 16-MAR-2000.
XX
PF 07-SEP-1999; 99MO-US20419.
XX
PR 08-SEP-1998; 98US-0099521.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
XX
PI Cahoon RE, Miao G, Powell W;
XX
DR WPI: 2000-256964/22.
DR N-PSDB; AA251792.
XX
PR New isolated polynucleotide encoding farnesyltransferase polypeptide is
PR useful for producing transgenic plants with an altered level of
PR farnesyltransferase -
PS
PS Claim 14; Page 41-42; 51pp; English.
XX
XX The present sequence is a farnesyltransferase beta subunit
CC from clone rlr24.pk0007.d6 isolated from rice infected leaf cDNA library
CC rlr24. The coding sequence of this protein is used in the construction
CC of a chimeric gene to produce transgenic plants with altered level
CC of farnesyltransferase subunit. Plants with decreased farnesyltransferase
CC activity may have enhanced tolerance to drought stress. Nucleic acids
CC encoding all or a part of farnesyltransferase proteins can be used in
CC studies to understand cell growth in plants and provide genetic tools to
CC control cell growth and improve tolerance to drought in mature plants.
XX
XX Sequence 313 AA:
SQ

Query Match 54.28; Score 1306; DB 21; Length 313;
Best Local Similarity 80.7%; Pred. No. 4,6e-125;
Matches 247; Conservative 24; Mismatches 25; Indels 10; Gaps 4;

OY 1 MDPSPSTPTGDDPA-----AAD--PDLRLVTGYEQKMFARVGDYRSLFGAP 52
DB 1 MDP-PSPPPPPPYPAAGSGPADSQAALPRLVTGYEQKMFARVGLFVFGAP 59
OY 53 NTKSIMLELRDQHIETLPGLRHNGPAFVLDANRPMCTGMVHPLALDEALDDLEN 112
DB 60 NANSIMLELRDQHIETLPGLRHNGPAFVLDANRPMCTGMVHPLALDE-IPDDVED 118
OY 113 DIIDPLARCDDKDGSGGPGQLPHLATTYAAVNTLWTIGSERALSSINRGILYFMQM 172
DB 119 DIVDFLRCDDKDGSGGPGQLPHLATTYAAVNTLWTIGSERALSSINRGILYFMQM 178
OY 173 KDVGARFMHGGGIDYRASATASVSLVNLIDFKLAGVDYIARCTGEGGAGRPY 232
DB 179 KDVGARFMHGGGIDYRASATASVSLVNLIDFKLAGVDYIARCTGEGGAGRPY 238
OY 233 AEAHGTYFCGLAALLILNLAEXVDPLSLIGWAFRGQVECGFQGRTNKLVGCGSFMWG 292
DB 239 AEAHGTYFCGLAALLILNLAEXVDPLSLIGWAFRGQVECGFQGRTNKLVGCGSFMWG 298
OY 293 AAIAFT 298
DB 299 AALALIT 304

RESULT 4
AAG10406
ID AAG10406 standard; Protein; 443 AA.
XX
AC AAG10406;
XX

DT 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 8715.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hydridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
XX
XX EPI033405-A2.
PN
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1998; 99US-0125788.
PR 25-MAR-1998; 99US-0126284.
PR 29-MAR-1999; 99US-0126785.
PR 01-Apr-1999; 99US-0127462.
PR 06-Apr-1999; 99US-0128234.
PR 08-Apr-1999; 99US-0128714.
PR 16-Apr-1999; 99US-0129845.
PR 19-Apr-1999; 99US-0130077.
PR 21-Apr-1999; 99US-0130449.
PR 23-Apr-1999; 99US-0130510.
PR 23-Apr-1999; 99US-0130891.
PR 28-Apr-1999; 99US-0131449.
PR 30-Apr-1999; 99US-0132048.
PR 30-Apr-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134236.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.

PR	18-JUN-1999	9905-0139716
PR	21-JUN-1999	9905-0139817
PR	22-JUN-1999	9905-0139999
PR	23-JUN-1999	9905-0140353
PR	24-JUN-1999	9905-0140354
PR	25-JUN-1999	9905-0140625
PR	26-JUN-1999	9905-0140893
PR	29-JUN-1999	9905-0140991
PR	30-JUN-1999	9905-0141387
PR	01-JUL-1999	9905-0141842
PR	02-JUL-1999	9905-0142154
PR	06-JUL-1999	9905-0142055
PR	08-JUL-1999	9905-0142390
PR	10-JUL-1999	9905-0142803
PR	12-JUL-1999	9905-0142927
PR	13-JUL-1999	9905-0143342
PR	14-JUL-1999	9905-0143624
PR	15-JUL-1999	9905-0144005
PR	16-JUL-1999	9905-0144086
PR	19-JUL-1999	9905-0144325
PR	19-JUL-1999	9905-0144332
PR	19-JUL-1999	9905-0144333
PR	19-JUL-1999	9905-0144334
PR	19-JUL-1999	9905-0144335
PR	20-JUL-1999	9905-0144352
PR	20-JUL-1999	9905-0144632
PR	20-JUL-1999	9905-0144684
PR	21-JUL-1999	9905-0144811
PR	21-JUL-1999	9905-0145086
PR	21-JUL-1999	9905-0145088
PR	22-JUL-1999	9905-0145085
PR	22-JUL-1999	9905-0145087
PR	22-JUL-1999	9905-0145089
PR	22-JUL-1999	9905-0145192
PR	23-JUL-1999	9905-0145148
PR	23-JUL-1999	9905-0145151
PR	23-JUL-1999	9905-0145524
PR	26-JUL-1999	9905-0145576
PR	27-JUL-1999	9905-0145513
PR	27-JUL-1999	9905-0145518
PR	27-JUL-1999	9905-0145519
PR	28-JUL-1999	9905-0145551
PR	02-AUG-1999	9905-0146386
PR	02-AUG-1999	9905-0146388
PR	02-AUG-1999	9905-0146589
PR	03-AUG-1999	9905-0147038
PR	04-AUG-1999	9905-0147204
PR	04-AUG-1999	9905-0147302
PR	05-AUG-1999	9905-0147492
PR	05-AUG-1999	9905-0147760
PR	06-AUG-1999	9905-0147703
PR	06-AUG-1999	9905-0147416
PR	09-AUG-1999	9905-0147933
PR	09-AUG-1999	9905-0147935
PR	11-AUG-1999	9905-0148171
PR	11-AUG-1999	9905-0148319
PR	12-AUG-1999	9905-0148361
PR	13-AUG-1999	9905-0148545
PR	13-AUG-1999	9905-0148684
PR	16-AUG-1999	9905-0149358
PR	17-AUG-1999	9905-0149175
PR	18-AUG-1999	9905-0149426
PR	20-AUG-1999	9905-0149722
PR	20-AUG-1999	9905-0149723
PR	23-AUG-1999	9905-0149902
PR	23-AUG-1999	9905-0149930
PR	25-AUG-1999	9905-0150566
PR	26-AUG-1999	9905-0150884
PR	27-AUG-1999	9905-0151065

PR	27-AUG-1999	99US-0151080
PR	27-AUG-1999	99US-0151086
PR	30-AUG-1999	99US-0151103
PR	31-AUG-1999	99US-0151130
PR	01-SEP-1999	99US-0151148
PR	07-SEP-1999	99US-0152363
PR	10-SEP-1999	99US-0153070
PR	13-SEP-1999	99US-0153758
PR	15-SEP-1999	99US-0154018
PR	16-SEP-1999	99US-0154039
PR	20-SEP-1999	99US-0154717
PR	22-SEP-1999	99US-0155131
PR	23-SEP-1999	99US-0155486
PR	24-SEP-1999	99US-0155589
PR	28-SEP-1999	99US-0156458
PR	29-SEP-1999	99US-0156566
PR	14-OCT-1999	99US-0157117
PR	05-OCT-1999	99US-0157753
PR	06-OCT-1999	99US-0157863
PR	07-OCT-1999	99US-0158029
PR	08-OCT-1999	99US-0158232
PR	12-OCT-1999	99US-0158269
PR	13-OCT-1999	99US-0159393
PR	13-OCT-1999	99US-0159294
PR	13-OCT-1999	99US-0159295
PR	14-OCT-1999	99US-0159329
PR	14-OCT-1999	99US-0159330
PR	14-OCT-1999	99US-0159331
PR	14-OCT-1999	99US-0159637
PR	14-OCT-1999	99US-0159638
PR	18-OCT-1999	99US-0159584
PR	21-OCT-1999	99US-0160741
PR	21-OCT-1999	99US-0160767
PR	21-OCT-1999	99US-0160768
PR	21-OCT-1999	99US-0160770
PR	21-OCT-1999	99US-0160814
PR	21-OCT-1999	99US-0160815
PR	22-OCT-1999	99US-0160980
PR	22-OCT-1999	99US-0160981
PR	22-OCT-1999	99US-0160982
PR	25-OCT-1999	99US-0161004
PR	25-OCT-1999	99US-0161405
PR	25-OCT-1999	99US-0161406
PR	26-OCT-1999	99US-0161359
PR	26-OCT-1999	99US-0161360
PR	26-OCT-1999	99US-0161361
PR	28-OCT-1999	99US-0161920
PR	28-OCT-1999	99US-0161922
PR	28-OCT-1999	99US-0161923
PR	28-OCT-1999	99US-0162142

[illegible]

PR	05-AUG-1999;	99US-0147260;
PR	06-AUG-1999;	99US-0147302;
PR	06-AUG-1999;	99US-0147416;
PR	09-AUG-1999;	99US-0147493;
PR	09-AUG-1999;	99US-0147935;
PR	10-AUG-1999;	99US-0148171;
PR	11-AUG-1999;	99US-0148319;
PR	12-AUG-1999;	99US-0148341;
PR	13-AUG-1999;	99US-0148565;
PR	13-AUG-1999;	99US-0148688;
PR	16-AUG-1999;	99US-0149368;
PR	17-AUG-1999;	99US-0149175;
PR	18-AUG-1999;	99US-0149426;
PR	20-AUG-1999;	99US-0149722;
PR	20-AUG-1999;	99US-0149723;
PR	20-AUG-1999;	99US-0149929;
PR	23-AUG-1999;	99US-0149902;
PR	23-AUG-1999;	99US-0149930;
PR	25-AUG-1999;	99US-0150360;
PR	26-AUG-1999;	99US-0150386;
PR	27-AUG-1999;	99US-0150884;
PR	27-AUG-1999;	99US-0151065;
PR	27-AUG-1999;	99US-0151066;
PR	30-AUG-1999;	99US-0151080;
PR	31-AUG-1999;	99US-0151303;
PR	31-AUG-1999;	99US-0151438;
PR	01-SEP-1999;	99US-0151930;
PR	07-SEP-1999;	99US-0152360;
PR	10-SEP-1999;	99US-0152383;
PR	13-SEP-1999;	99US-0153070;
PR	15-SEP-1999;	99US-0153758;
PR	16-SEP-1999;	99US-0154018;
PR	20-SEP-1999;	99US-0154039;
PR	22-SEP-1999;	99US-0154779;
PR	23-SEP-1999;	99US-0155139;
PR	24-SEP-1999;	99US-0155486;
PR	28-SEP-1999;	99US-0156455;
PR	29-SEP-1999;	99US-0156596;
PR	04-OCT-1999;	99US-0157111;
PR	05-OCT-1999;	99US-0157753;
PR	06-OCT-1999;	99US-0157865;
PR	07-OCT-1999;	99US-0158029;
PR	08-OCT-1999;	99US-0158232;
PR	12-OCT-1999;	99US-0158369;
PR	13-OCT-1999;	99US-0159299;
PR	13-OCT-1999;	99US-0159299;
PR	13-OCT-1999;	99US-0159299;
PR	14-OCT-1999;	99US-0159329;
PR	14-OCT-1999;	99US-0159330;
PR	14-OCT-1999;	99US-0159331;
PR	14-OCT-1999;	99US-0159637;
PR	14-OCT-1999;	99US-0159638;
PR	18-OCT-1999;	99US-0159584;
PR	21-OCT-1999;	99US-0160741;
PR	21-OCT-1999;	99US-0160767;
PR	21-OCT-1999;	99US-0160768;
PR	21-OCT-1999;	99US-0160770;
PR	21-OCT-1999;	99US-0160814;
PR	21-OCT-1999;	99US-0160815;
PR	22-OCT-1999;	99US-0160980;
PR	22-OCT-1999;	99US-0160981;
PR	22-OCT-1999;	99US-0160989;
PR	25-OCT-1999;	99US-0161404;
PR	25-OCT-1999;	99US-0161405;
PR	25-OCT-1999;	99US-0161406;
PR	26-OCT-1999;	99US-0161359;
PR	26-OCT-1999;	99US-0161360;
PR	26-OCT-1999;	99US-0161361;
PR	28-OCT-1999;	99US-0161920;
PR	28-OCT-1999;	99US-0161992;
PR	28-OCT-1999;	99US-0161993;
PR	29-OCT-1999;	99US-0162142;

Best Local Similarity 51.7%: Pred No. 1,96-114,
Matches 232; Conservative 73; Mismatches 111; Indels 33; Gaps 3;

```
OY      22 DLPLRYTVOYOMKVEARVDIYRSLFGAAPNTKSIMLEMRQHIIEYLPGRHNGPAF 81  
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db      35 ELSSITVSORBOEFLVENDYVGIIYNFEADSDYSTOKYMEIORKDLDYLMKGRLQGP 94  
  
OY      82 HVLDAENPMICVMNVHPILALDLBADDDLENDIIDFLARCODRKGGYSGGPGOLPHLATTT 141  
       |||||||::|::||::||::||::||::||::||::||::||::||::||  
Db      95 SSLDANRPMLCYMIHLNISIALGLFTYVDDLESNALDFLRCGGSSCGTGPGOLPHLATTT 154  
  
OY      142 YAAVNTLVTTGSERALSINRNKLYNFMLOMKDVSGAFRMHDGEIDVRASYAISVASL 201  
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db      155 YAAVNAVLVTTCGSKALSIINREKMSCFLRMKDTISGGFRMHDGELDIVRACYAISVASI 214  
  
OY      202 VNIDPFKLAVGVGDYTLARCOTEGGJAGEPYVAEAHGVTTEGCIALTLINAEKVDPSTL 261  
       ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db      215 LNIHDELDTGCLGDIYLSCOTYEGLIGEPGSEAHGTYTGGLAAMLIENDRMDLSL 274  
  
OY      262 IGVAFPRGVCECFQRRTKNLYDGCSFWOGAALAFTOKLTITYDKQLSYSSCKR--- 317  
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db      275 MNMAVHRQGVEMGFQGRTKMYLGDGYTFWQAAPCVLLRLSTNDHDVHGSSHISEGTNE 334  
  
OY      318 -----PSGEDACSTSSYCGCTAKKSSSAVDYAFCGPDFIOGSNOIGPLF 360  
       ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db      335 EHNAHDEDDLIEDDDDDDEDNEDSVNGRIHTST-----YINRMQL--VF 382  
  
OY      361 HNIAAQYYITLCQVLEBGLRDPKGNRDTHSCYCISGLAVSOYSAMTDGSCPLOHY 420  
  
Db      363 DSLGLRGYVLLCKIRDPGERDKPRPDRFYHTCYCISGLSVAOHAWLKDEDIPPLTRDI 442  
  
OY      421 LGPYSNLLEPIHPLNYNVLDKRYHTAYEEFF 449  
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db      443 MGYSNLEPVPOLLHNIVMDQYNEAIEEFF 471
```

RESULT 6
AAG46813
ID AAG46813 standard; Protein; 444 AA.
XX AAC46813;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58934.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PM EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 200DEP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134376.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139753.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140635.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142380.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144086.
PR 16-JUL-1999; 99US-0144085.
PR 19-JUL-1999; 99US-0144335.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145182.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 26-JUL-1999; 99US-0145224.
PR 27-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147280.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147453.
PR 09-AUG-1999; 99US-0147935.
PR 11-AUG-1999; 99US-0148171.
PR 12-AUG-1999; 99US-0148319.
PR 13-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149920.
PR 23-AUG-1999; 99US-0149920.
PR 25-AUG-1999; 99US-0149920.
PR 26-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151920.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154039.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0156559.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.

OY 420 VLGPYSNLEPIPIPLYNVLDKHTAYEFF 449
DB 443 IMGYSNLEPIQVLHNTVMQYNEATEFF 472

RESULT 8
AAG10407
ID AAG10407 standard; Protein: 405 AA.
XX AAG10407;
XX
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8716.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
XX
PN EPI03405-A2.
PD
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123568.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126284.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134286.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134370.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135114.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137358.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138867.
PR 14-JUN-1999; 99US-0139219.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140981.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.

```

PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156595.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match      48.38; Score 1163.5; DB 21; Length 405;
Best Local Similarity 53.08; Pred. No. 2.8e-110;
Matches 219; Conservative 68; Mismatches 93; Indels 33; Gaps 3;

```

```

QY 178 AFRMHGGEIDVRASVTASLVNLTDFRLKANGVDYIARCOYEGGJNAGEPYAEANG 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GRRMHGGEIDVRASVTASVTASLTNIMDELTGGLADYILSCQYIEGGJGGEPSSEANG 180
QY 238 GTTFGGLAALLILNFAEKVDPSSLIGWAFRQVCEGFGQRTNKLVDGYSFMOGAAIAF 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GTYCGGLAAMTILNEVDRILNDSILMNWAVHROGVEGFGQRTNKLVDGYSFMOGAAIAF 240
QY 298 TQKLITVDKQKSSYSOKR-----PGGEACTSSYGCSTAKKS 336
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 LQRLYSTNDHDVGHSSHISEGTNEHHNHDDEDDLESDDDDDDDDDSDNDSDVNGRIHTT 300
QY 337 SSADVAKAFGEFDIQSQNIGPLFNHIALQOYILLCQVLEGLRDKPKNBDHYHSCYC 396
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 ST-----YINRRQQL--VFDISGLQRYVLLCSKIPDGGFRDKPRKPRDPYHTCYC 348
QY 397 LGLAVSOYSAMTDGSCPLPOHVLGPRSNLPEHPLVNVLDKXHTAYEERF 449
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 349 LGLSVQAHAMLKEDPTPLTRDIMGYSNLEEVQILNHTVMDQYNEAIEFF 401

RESULT 9
AAW97867
ID AAW97867 standard; Protein; 404 AA.
XX
AC AAW97867;
XX
DT 07-JUN-1999 (first entry)
XX
DE Arabidopsis farnesyl transferase.
XX
KW Farnesyl transferase; ERAL gene; transgenic plant;
KM stress tolerance; cold tolerance; drought tolerance;
KW salt tolerance; senescence.
XX
OS Arabidopsis thaliana.
XX
PN W09906580-A2.
XX
PD 11-FEB-1999.
XX
PF 29-JUL-1998; 98MO-US15664.
XX
PR 01-AUG-1997; 97US-0054474.
XX
(PEPF-) PERFORMANCE PLANTS INC.
XX
PA Bonetia D, Cutler S, Ghassemian M, McCourt P;
PI WPI: 1999-153807/13.
PI N-PSDB: AAX24384.
DR
DR New isolated Arabidopsis farnesyl transferase gene - used to develop
PT plants having improved stress tolerance, altered lateral branching,
PT delayed senescence or altered flowering numbers
PT
PT Claim 4; Fig 2; 66pp; English.
PS
PS
XX
XX This is the amino acid sequence of the farnesyl transferase (FT)
CC encoded by the ERAL gene (see AAX24384) of Arabidopsis thaliana. FT
CC is involved in the regulation of lateral branching, regulation of
CC the response to abscisic acid (ABA) and regulation of senescence.
CC A claimed nucleic acid construct comprises a promoter and a
CC nucleic acid encoding an inhibitor of a plant FT. Such constructs
CC can be used to produce plants having improved tolerance to drought,
CC salt and cold stress, reduced lateral branching, delayed senescence
CC and increased numbers of flowers. Also claimed in a seed, plant
CC part, cell or tissue culture or regenerated transgenic plant
CC containing the claimed nucleic acid construct, the plant being a
CC monocot or dicot, especially a Brassica sp. A plant having a
CC mutation in the ERAL gene that results in loss of FT activity is
CC also claimed.

```

```
XX Sequence 404 AA;
SQ
Query Match 48.1%; Score 1159.5; DB 20; Length 404;
Best Local Similarity 52.9%; Pred. No. 7.2e-110;
Matches 218; Conservative 66; Mismatches 93; Indels 33; Gaps 3;

OY 59 LELMRDNIETVLPGLRMGPAFVFLDANRPMCLYMWVHPLALLDEALDDLENDIDFL 118
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 1 MEIQRDRKLDYLMKGLRQLGPGFSSLDANRPMCLYWIHSIALGETVDELESNAIDPL 60

OY 119 ARGQKDGSGSGGPGQLPLATTTAAVNTLVTTGSEBALSSINRGVLNFMLOMKDVSGA 178
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 61 GRCQSGEGGSGGPGQLPLATTTAAVNTLVTTGSDALSSINRMSCFLRMKDTSGG 120

OY 179 FRMHDCGEIDVNASYTAISVALNVIDFLKAGVDYIARCOYEGEIGAGEPYAEANGC 238
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 121 FRMHDCGEIDVACYTAISVASIINIMDELTGGLDGYILSCQYEGGIGGEGSEANGC 180

OY 239 YTEFGGLALLILNEAEKVDLPILGNVAFRGVCEGCGPGRTNKLVNCGCSFPGGAIAFT 298
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 181 YTYCGLAAILINEVDRLNLDLSLMMMAVHRQGVEMGFGCKTNLVGCTTFWQAPCYLL 240

OY 299 QRLITVKKQLKSSYCKR-----PSGEDACSTSYGCTAKKSS 337
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 241 ORLYSTNDHDVHGSSHISEGTNEEHHAHDEDDLEDSDDDSDSDSDNDPDSVGNHRIHTS 300

OY 338 SAVDVAKGCFDFIIOOSNGICPLFNIALQYILLCGVLGCRDKRGKNRDHYSCYCL 397
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 301 T-----YINRMQL--VFDSLGDRIVLCSLETPDGGFRDPRKPRDPYIACYCL 348

OY 398 SGLAVSOYSAMDTGSCPLPQHVLGPPYSNLEPRLPYNVVLDKYHTAVEFF 449
   ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 349 SGLVAQHAKMLKDEDTPLTRDIMGYCSNLEPYQLLNINVMQYNEAIEFF 400

RESULT 10
AAC46814
ID AAC46814 standard; Protein: 406 AA.
XX
AC AAC46814;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58935.
XX
KM Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126284.
PR 29-MAR-1999; 99US-0126285.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 16-APR-1999; 99US-0128714.
PR 19-APR-1999; 99US-0129845.
PR 21-APR-1999; 99US-0130077.
PR 23-APR-1999; 99US-0130049.
PR 23-APR-1999; 99US-0130310.
PR 28-APR-1999; 99US-0130891.
PR 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132483.
PR 11-MAY-1999; 99US-0134216.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136393.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137502.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138647.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139889.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142350.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144335.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
```


PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145192.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149920.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158322.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
XX

PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
XX

Query Match 47.7%; Score 1150; DB 21; Length 406;

Best Local Similarity 52.7%; Pred. No. 6, 8e-109; Mismatches 93; Indels 34; Gaps 4;

Matches 218; Conservative 69; Mismatches 93; Indels 34; Gaps 4;

QY 58 MLELRDQHEIYLPGLRHMGPAFHYLDANRPMLCYWVHPALALDEALDDLENDIIDF 117

DB 1 MMEIQRKQLDLYLKMGLRQGLQFSSLDANRPMLCYWILHSIALGFTVDELSNADIF 60

QY 118 IARCDKRGCGYSGRGOLPHLATTYAAVNTLVYTSGERLSSIN-RGMLYNPMLDMKDV 176

DB 61 LGRCGSGGCGYGGGPGOLPHLATTYAAVNALVLYLGGDKLSSINERKMSGLRKMOTS 120

QY 177 GAFRMDGEIDVRASTYATISVASLVNIDFKLAKGVGDYIARCOTYEGGIAGEPYAEH 236

DB 121 GGFRRHDMGEMDVACYTATISVASILNIMDELTQGLIGDYILSCQTYEGGIGGEGPSAH 180

QY 237 GGYTFCGIALILINLEAKVDLSLIGVAFRCGVCSCGSGTNTLVGCSYFPGAGALA 296

DB 181 GGYTGGGLAMLILNEVDRLKLSLMMNAVHROGVEMGFGKRTNKLVDGCTTFPOACV 240

QY 297 FTQKLITVDKQLKSSYSCKR-----PSGEDACSTSSYGCTAKK 335

DB 241 LLORLYSTNDHDVHSGSHISEGTNEEHAHDEDELDSDDDSDSDSDSDSVNCHRIH 300

QY 336 SSSAVDAKFCGDFLIQSONOIGPLFNIALDOYIILCSOVLBGLRDKPKNRDHYSCY 395

DB 301 TST-----YINRMOL--VFDSLGLOKIVLLCSXIPDGGFRDKPRKPRDFYHTCY 348

QY 396 CUSGLAVSQYSAMTDTGSCPLPQHVILGYPYSNLLEPIPLVNVLDKRYHTAYEFP 449

DB 349 CUSGLVAGHAKLDEDEPTLRIDIMGYSNLEPOLLHNIMQVNEALEIFF 402

RESULT 11

AAK54829
ID AAK54829 standard; Protein; 437 AA.

AC AAK54829;

DT 07-NOV-1994 (first entry)

DE Beta subunit of bovine brain FPPase.

KW Farnesyl protein transferase; inhibition; farnesylation.

XX Bos taurus.

OS W09410184-A.

XX 11-MAY-1994.

PD 29-OCT-1993; 93MO-US10442.

XX


```
AA07840      AA07840 standard;Protein; 437 AA.  
XX ID   AA07840:  
XX AC  
XX XX  
XX XX  
XX D7    23-JAN-1996 (first entry)  
XX DE     Rat farnesyl protein transferase beta subunit.  
XX KW     Farnesyl transferase; inhibitor; cancer; ras; p21.  
XX RV     Rattus sp.  
PN PN     US5420245-A.  
PD PD     30-MAY-1995.  
XX XX  
PP PP     18-APR-1990;       90US-0510706.  
PR PR     16-JAN-1992;       92US-0822011.  
PR PR     18-APR-1990;       90US-0510706.  
PR PR     20-NOV-1990;       90US-0615715.  
PR PR     03-APR-1992;       92US-0863169.  
PA PA     (TEXA ) UNIV TEXAS.  
PX PX  
PI PI     Brown MS, Goldstein JL, Reiss Y;  
DR DR     WP1: 1995-206308/27.  
NR NR     N-PDSB: AAQ94411.  
PT PT     New farnesyl transferase inhibitor peptide(s) - based on farnesyl  
PT acceptor substrate carboxy terminal sequences, used for the  
PS PS     treatment of cancer  
  
Example 3: Column 51-53: 55pp; English.
```

AA07840 is the beta subunit of rat farnesyl transferase which is involved in the farnesylation of various cellular proteins including the cancer related ras proteins. It is used to produce the complete farnesyl transferase molecule which is used to demonstrate the effectiveness of peptide inhibitors capable of inhibiting farnesyl transfersases. The peptide inhibitors are useful for treating cancers and ras-related cancers in particular.

Sequence 437 AA:

Query Match 39.1%; Score 942.5; DB 16; Length 437;

Best Local Similarity 43.1%; Pred.No.1,4e-87;

Matches 197; Conservative 64; Mismatches 137; Indels 59; Gaps

Y 5 POSRPPTGGDPAAPAADPLP-----LTYTVEBKVKVARGDIIYSLFGAARPKS 56
| | : : . : . : | : | | | | | : : : |
DB 12 PSSSPWSESLTLREHARRERLDODSYETLSQAKEKQEVSST--KENHLV 68
| | : : . : . : | | | | | | : : : |
Y 57 IMELMRDOIEIYLTPGLRLRHGAFHVLDANKRWICVMMPILALDLPEADDLENDIID 116
| | : : . : . : | | | : : : | | | | : : |
DB 69 PRTVLGRKHFFHYLRKGROLTDVAEBCDLSRRPWLCYWMLSHLEDDEIPQLAVTVDCQ 128
| | : : . : . : | | | | | | : : : |
Y 117 FLACCPDKCGYGSGGCOLPHLTATYAANTLVTTIGSERALLSNRCNLNFMLOAKDVIS 176
| | : : . : . : | | | | | | : : : |
DB 129 FLELCQGSDPGGSFGGEQYPHALPYAAAVALCTITGEAEYNVINRKLLQVIYSTLKQP 188
| | : : . : . : | | | | | | : : : |
Y 177 GAFRMHGGEIDIRASTAYSASLVNIIDEFLAKGVGYDIARCOTYEAGIAGEPYAEA 236
| | : : . : . : | | | | | | : : : |
DB 189 GSFLMHWGCDEVDRSAACAASYALSNTITPDLFEGTAEMTIARCONNEGIGVGMEAH 248
| | : : . : . : | | | : : : | | | | : : |
Y 237 GGTFEEGLAILLIINRAEKVDLP SLTGAWAFNQ-CVEEGPCGGRNKTVLDVCYSFGOGAAL 295
| | : : . : . : | | | | | | : : : |
DB 249 GGTFEEGLAIIVLIKERSLNLSKLQMTWTSMQNRFEEGFGRCKTKLDVGTSFWMG-- 306
| | : : . : . : | | | | | | : : : |
Y 296 AFNGKITIVDKOLSSKYSCKRPEGEDACTSVSYCSTA KSSASAVIDYAKFGDFEQIQSNG 355
| | : : . : . : | | | | | | : : : |

```

Db 307 ---LLPLRLALHA-----QGDPAISMSH----- 328
OY 356 IGPLFHNIALQOYILLCSQVLEGSLRDRPKNRDHYHSCYCLSGLAVOYSAMTDTGSCP 415
Db 329 ---FHHOALQDEYILKCCOCPCAGGLDRKRSRPFYHRCYCLSLGSLIAOHFG----SGAM 381
OY 416 LPOHVLGPNYSNLEPIHPLYNVLVDKRYHAYKEFPSEE 452
Db 382 LHDVYMGVPENVLQPTHVPYINIGPKVIQATTHLEOK 418

RESULT 14
AAW04428
AAW04428 standard: Protein: 437 AA.
AAW04428:
AC AAW04428:
XX
XX
XX 30-JUL-1997 (first entry)
DE Rat farnesyl transferase enzyme beta subunit.
XX
XX Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;
KW ras protein; K-ras B; malignant; detection; identification.
XX
XX Rattus rattus.
XX OS
XX MO9634113-A2.
XX PN
XX PD 31-OCT-1996.
XX PF 29-APR-1996; 96WO-US05969.
XX PR 27-APR-1995; 95US-0429964.
XX PT
XX PT (TEXA ) UNIV TEXAS SYSTEM.
PA
PI Brown MS, Goldstein JL, James GL;
XX
XX WPI: 1996-497642/49.
DR N-PSDB; AAT8709.
XX
XX Assay for farnesyl transferase activity - by determining ability to
PT transfer farnesyl moiety to K-ras B protein, partic. useful for
PT identifying inhibitors
XX
XX Example 3; Page 143-147; 257pp; English.
XX
XX AAW04428 shows the beta subunit of a farnesyl transferase (FT) enzyme
CC derived from rat brain tissue. The enzyme was used in a method
CC for identifying FT inhibitors. The method involved screening candidate
CC compounds for the ability to inhibit the transfer of a farnesyl moiety
CC to a K-ras B protein. FT inhibitors act by blocking the attachment of
CC prenyl groups to ras proteins in malignant cells of patients suffering
CC from cancer or precancerous states, and as such are used to treat such
CC conditions.
XX
XX
XX Sequence 437 AA:

Query Match 39.1%; Score 942.5; DB 17; Length 437;
Best Local Similarity 43.1%; Pred. No. 1.4e-87;
Matches 197; Conservative 64; Mismatches 137; Indels 59; Gaps
OY 5 POSTPTGDDPAAADPDLEPR-----LAVTOVEOMKVEARVDIYRSLFGAADNTRK 56
Db 12 PSSSPVMSPEPLSLRPEHARERLQDDSVETVTSIEOKAVEKIOEVFSY--KFNHLV 68
OY 57 IMELMMDHDIETLTGTIRHMGPARFHVLDANPMICYMMVPIALALDEALDDLENDIID 116
Db 69 PRLVLOKEHFHFLKRLKGLDTDAIECDASHPMVLCVILMSLELDEPIPOIVATVDQC 128
OY 117 FLARCQDKGSGGSGFQQLPHATTAAVNTLVLTIGSERALSSINRGNLVNFMLQKDV 176
Db 129 FLELCSPDGGFGGSGFQGYPHLAPTYAAVNALCIITGEAVNVINREKLLQYLYSLKOPD 188

```

QY 177 GAFRHHGGEIDVRASTYATISVASLVNILDPKLAKGVGYIARCOTTEGGIAGEPYAEAH 236
 DB 189 GSFLLHVGGEVDVRSAYCAASVASTLITPDLFEGETAEIARCQWMEGGIGVGMENH 248
 QY 237 GGTFECGLAALILNEAEKVDLPSLIGVAFRQ-GVECGFGRTNKLVDGCTSFMOGAII 295
 DB 249 GGTFECGLAALVILKRESLNLSLQWMTSRQMRFGGFGGRCKNLVDGCTSFMOAG-- 306
 QY 296 APTOKLITITVDKOLKSSYSCRRPGEEDACTSSYCTAKKSSAANDYAFGDFIQOSNQ 355
 DB 307 -----LPLHLHRAHA-----OGDPALSMSHW----- 328
 QY 356 IGPLFHNIADQYIILCSQVLEGLRDKPGKNDHYHSCYCLSGLAVSQYSAMTDGSCP 415
 DB 329 ---MFHQOALQEYILMCCQCPAGGLDLPKPSRDFHTCYCLSLIAOHFG---SGAM 381
 QY 416 LPQHVIGPYSNLPEIHPILYVNVLDKXHTAYEEFSEE 452
 DB 382 LHDVYGVPEVNLQPTHPVNIIGPKVYIQATTTFLQK 418

 RESULT 15
 AARS4831
 ID AARS4831 standard; Protein: 437 AA.
 AC AARS4831;
 XX
 DT 07-NOV-1994 (first entry)
 XX
 DE Beta subunit of human FPPase.
 XX
 KW Farnesyl protein transferase; Inhibition: farnesylation.
 XX
 OS Homo sapiens.
 XX
 PN W09410184-A.
 XX
 PD 11-MAY-1994.
 XX
 PF 29-OCT-1993; 93WO-US10442.
 XX
 PR 30-OCT-1992; 92US-0968782.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Diehl RE, Glabbs JB, Kohl NE, Omer CA;
 XX
 DR WPI: 1994-167373/20.
 DR N-PSDB: AA064888.
 XX
 PT Mammalian farnesyl protein transferase produ. - used in assays
 PT for cpds. with inhibitory activity for the identification of
 PT anticancer agents
 PS
 PS Disclosure: fig 3; 69pp: English.
 XX
 CC The cDNA encoding the human beta subunit of FPPase was isolated
 CC from a human placental cDNA library in lambda gtl1 using a bovine
 CC FPPase cDNA probe. The FPPase can be used to assess the inhibitory
 CC activity of a cpd. in the farnesylation of a protein substrate.
 CC The assay can be used to identify anticancer agents.
 CC See also AARS4829-32.
 CC
 XX
 SQ Sequence 437 AA:

Query Match 39.0%; Score 940.5; DB 15; Length 437;
 Best Local Similarity 43.1%; Pred. No. 2,3e-87;
 Matches 197; Conservative 62; Mismatches 139; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAAADPDLPR-----LTVQVEQMKVEARVGDIVRSIFGAAPNTRKS 56
 DB 12 PSSSPVSWSEPLYSIRPEHARERLQDDSVETVTSIRQAKVEEKIQEVFSSY---KFNHLV 68

QY 57 IMLEIMRQDNIETLTPGIRHNGPAFHVLDANRPWLCYMWVHPLALIDEALDDLENDIID 116
 DB 69 PRLVLDORRKHNRHYLKRGRLOLTDAYECLDASRPMWLCYWIHLSLELLEDEIPQIVATDVCO 128
 QY 117 FLARCQDDGYSGGPGOLPHLATTYAANTLVITIGSERALSSINRGNLYNFMLOMKDVS 176
 DB 129 FLELDQSPDEGGGPGQYRHLAPTAAVNAALCIIGTEEAYDIINREKLDQVLSLQKPD 188
 QY 177 GAFRHHGGEIDVRASTYATISVASLVNILDPKLAKGVGYIARCOTTEGGIAGEPYAEAH 236
 DB 189 GSFLLHVGGEVDVRSAYCAASVASTLITPDLFEGETAEIARCQWMEGGIGVGMENH 248
 QY 237 GGTFECGLAALILNEAEKVDLPSLIGVAFRQ-GVECGFGRTNKLVDGCTSFMOGAII 295
 DB 249 GGTFECGLAALVILKRESLNLSLQWMTSRQMRFGGFGGRCKNLVDGCTSFMOAG-- 306
 QY 296 APTOKLITITVDKOLKSSYSCRRPGEEDACTSSYCTAKKSSAANDYAFGDFIQOSNQ 355
 DB 307 -----LPLHLHRAHA-----OGDPALSMSHW----- 328
 QY 356 IGPLFHNIADQYIILCSQVLEGLRDKPGKNDHYHSCYCLSGLAVSQYSAMTDGSCP 415
 DB 329 ---MFHQOALQEYILMCCQCPAGGLDLPKPSRDFHTCYCLSLIAOHFG---SGAM 381
 QY 416 LPQHVIGPYSNLPEIHPILYVNVLDKXHTAYEEFSEE 452
 DB 382 LHDVYGVPEVNLQPTHPVNIIGPKVYIQATTTFLQK 418

Search completed: November 1, 2002, 18:07:17
 Job time : 52 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2002, 18:07:56 ; Search time 19 Seconds

(without alignments)
581.072 Million cell updates/sec

Title: US-09-786-675-12

Perfect score: 2411
Sequence: 1 MDSPSTPTPTGDDPAAD.....PLYNVLDKHYTAEFFSEE 452

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: Issued Patents.AA:*
2: /cgn2.6/prodata/2/1aa/5A.COMB.pep:*
3: /cgn2.6/prodata/2/1aa/5B.COMB.pep:*
4: /cgn2.6/prodata/2/1aa/6A.COMB.pep:*
5: /cgn2.6/prodata/2/1aa/6B.COMB.pep:*
6: /cgn2.6/prodata/2/1aa/PCRTUS.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	942.5	39.1	437 1	US-07-863-169A-3 Sequence 3, Appl1
2	942.5	39.1	437 2	US-08-429-964-3 Sequence 3, Appl1
3	942.5	39.1	437 3	US-07-935-087-3 Sequence 3, Appl1
4	942.5	39.1	437 5	PCT-US93-08062-3 Sequence 3, Appl1
5	940.5	39.0	437 5	US-08-424-268-10 Sequence 10, Appl1
6	940.5	39.0	437 5	PCT-US93-10442-10 Sequence 10, Appl1
7	940.5	39.0	819 2	US-08-424-268-20 Sequence 20, Appl1
8	940.5	39.0	819 5	PCT-US93-10442-20 Sequence 20, Appl1
9	939.5	39.0	437 2	US-08-424-268-6 Sequence 6, Appl1
10	939.5	39.0	437 5	PCT-US93-10442-6 Sequence 6, Appl1
11	931.5	38.6	444 3	US-07-935-087-7 Sequence 7, Appl1
12	898.5	37.3	387 1	US-07-863-169A-7 Sequence 7, Appl1
13	898.5	37.3	387 2	US-08-429-964-7 Sequence 7, Appl1
14	898.5	37.3	387 5	PCT-US93-08062-7 Sequence 7, Appl1
15	359	14.9	355 4	US-09-387-574-8 Sequence 8, Appl1
16	359	14.9	355 4	US-09-668-096-8 Sequence 8, Appl1
17	320	13.3	377 1	US-08-188-277B-4 Sequence 4, Appl1
18	320	13.3	377 2	US-08-429-964-78 Sequence 78, Appl1
19	313	13.0	377 1	US-08-188-277B-2 Sequence 2, Appl1
20	313	13.0	377 2	US-08-429-964-80 Sequence 80, Appl1
21	304.5	12.6	313 4	US-09-387-574-4 Sequence 4, Appl1
22	304.5	12.6	313 4	US-09-668-096-4 Sequence 4, Appl1
23	291.5	12.1	318 4	US-09-387-574-2 Sequence 2, Appl1
24	291.5	12.1	318 4	US-09-668-096-2 Sequence 2, Appl1
25	285	11.8	281 4	US-09-387-574-6 Sequence 6, Appl1
26	285	11.8	281 4	US-09-668-096-6 Sequence 6, Appl1
27	97	4.0	1090 4	US-09-346-237-5 Sequence 5, Appl1

28	96.5	4.0	2703 1	US-08-185-433-19 Sequence 19, Appl1
29	90	3.7	343 4	US-09-193-503B-1 Sequence 1, Appl1
30	90	3.7	579 2	US-08-864-224-11 Sequence 11, Appl1
31	90	3.7	781 4	US-09-193-503B-3 Sequence 3, Appl1
32	90	3.7	781 4	US-09-193-503B-6 Sequence 6, Appl1
33	90	3.7	781 4	US-09-193-503B-9 Sequence 9, Appl1
34	90	3.7	781 4	US-09-193-503B-11 Sequence 11, Appl1
35	89.5	3.7	334 3	US-08-883-526-4 Sequence 4, Appl1
36	89.5	3.7	334 3	US-08-870-529-2 Sequence 2, Appl1
37	86	3.6	1298 4	US-08-690-473-2 Sequence 2, Appl1
38	86	3.6	1298 4	US-09-259-821A-2 Sequence 2, Appl1
39	86	3.6	1298 4	US-08-843-659-2 Sequence 2, Appl1
40	84.5	3.5	558 4	US-09-148-680-2 Sequence 2, Appl1
41	84	3.5	334 3	US-09-120-365-64 Sequence 64, Appl1
42	84	3.5	334 4	US-09-515-039-64 Sequence 64, Appl1
43	83	3.4	461 4	US-09-122-210-2 Sequence 2, Appl1
44	83	3.4	461 4	US-09-443-681-2 Sequence 2, Appl1
45	82	3.4	3066 4	US-08-952-127-12 Sequence 12, Appl1

ALIGNMENTS

RESULT 1
US-07-863-169A-3
Sequence 3, Application US/07863169A
Patent No. 5420245
GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: Tetrapeptide-Based Inhibitors of Farnesyl
TITLE OF INVENTION: Transferrase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/863,169A
FILING DATE: 03-APR-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/822,011
FILING DATE: 19-JAN-1992
CLASSIFICATION: 530
APPLICATION NUMBER: US 07/937,893
FILING DATE: 18-APR-1991
CLASSIFICATION: 530
APPLICATION NUMBER: US 615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 530
APPLICATION NUMBER: US 510,706
FILING DATE: 18-APR-1990
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:297/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

```

; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-863-169A-3

Query Match          39.1%; Score 942.5; DB 1; Length 437;
Best Local Similarity 43.1%; Pred. No. 2.8e-96;
Matches 197; Conservative 64; Mismatches 137; Indels 59; Gaps 7;

QY 5 POSTPTDDDDAAADPLR-----LTVOQOMKVEARVDIYRSLFGAARNKS 56
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 12 PSSSPVSEPLYSLRPHAREKLODDSVETVSIQAVEKEIDVFSY---KFNLY 68
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 57 IMLEWRDQHEIYLTPLGRHMGPAFHVLDANRPWLCYMWVHPLALLDEALDDLENDIID 116
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 69 PRLVQREKREHRYLKRGLRQLTDAVECLDASRPWLCYWLHSLLELLEDEPIQVATDVQC 128
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 117 FLARCDDGSGGPGOLPHLATYAAVNTLVLTIGSERALSSINRGNYNMLQMKDVS 176
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 129 FLELCQSPDGGFGGPGQYPLAPTYAAVVALCITIEAYVYINREKLLQTLVSLKQPD 188
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 177 GAFRNDGCEIDVRASTYASVSLVNIIDFKLAKGVGYIARCQTEGGIAGEPYAEAH 236
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 189 GSFLMHVGEVDVRSAYCAASVASTLTIITPDLEGTAEIARCONMEGIGVPGMEAH 248
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 237 GGYTCGALAILLNEAEKVDLPFLIGVAFRO-GVECGFQGRTKKLVDCGYSFMOGAII 295
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 249 GGYTCGALAILLNEAEKVDLPFLIGVAFRO-GVECGFQGRTKKLVDCGYSFMOGAII 306
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 296 AFTQKLITIVDKLSSYSCKRPSGEDACTSSYGCTAKKSSANDYAKFGDFIQOSNQ 355
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 307 -----LPLRLRALHA-----OGDPALSMSHW----- 328
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 356 IGPFHNALQOYIILCSQVLEGLRDKPGKNDYHSCYCLGSLAVSQYSAMDTGSCP 415
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 329 ---MFHQALQDEYILMCCQCPAGGLDKPKSRDFYHTCYCLSGLSINQHG----SGAM 381
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 416 LPQHVLPYSNLEPIHPLVNVVLDKHTAYEFSSSE 452
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 382 LHDVVMGVPENVLPQTHPVYVIGDPKVIAQTHTFLQK 418
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
US-08-429-964-3
; Sequence 3, Application US/08429964
; Patent No. 5962243
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: REISS, YUVAL.
; APPLICANT: JAMES, GUY L.
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
; TITLE OF INVENTION: TRANSFERASE INHIBITORS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08429,964
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,625
```

```

; FILING DATE: 16-FEB-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/822,011
; FILING DATE: ABANDONED
; CLASSIFICATION: 435
; APPLICATION NUMBER: PCT/US/91/02650
; FILING DATE: 18-APR-1991
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/615,715
; FILING DATE: 20-NOV-1990
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/510,706
; FILING DATE: 18-APR-1990 (ABANDONED)
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, DAVID L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:432/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-429-964-3

Query Match          39.1%; Score 942.5; DB 2; Length 437;
Best Local Similarity 43.1%; Pred. No. 2.8e-96;
Matches 197; Conservative 64; Mismatches 137; Indels 59; Gaps 7;

QY 5 POSTPTDDDDAAADPLR-----LTVOQOMKVEARVDIYRSLFGAARNKS 56
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 12 PSSSPVSEPLYSLRPHAREKLODDSVETVSIQAVEKEIDVFSY---KFNLY 68
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 57 IMLEWRDQHEIYLTPLGRHMGPAFHVLDANRPWLCYMWVHPLALLDEALDDLENDIID 116
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 69 PRLVQREKREHRYLKRGLRQLTDAVECLDASRPWLCYWLHSLLELLEDEPIQVATDVQC 128
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 117 FLARCDDGSGGPGOLPHLATYAAVNTLVLTIGSERALSSINRGNYNMLQMKDVS 176
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 129 FLELCQSPDGGFGGPGQYPLAPTYAAVVALCITIEAYVYINREKLLQTLVSLKQPD 188
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 177 GAFRNDGCEIDVRASTYASVSLVNIIDFKLAKGVGYIARCQTEGGIAGEPYAEAH 236
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 189 GSFLMHVGEVDVRSAYCAASVASTLTIITPDLEGTAEIARCONMEGIGVPGMEAH 248
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 237 GGYTCGALAILLNEAEKVDLPFLIGVAFRO-GVECGFQGRTKKLVDCGYSFMOGAII 295
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 249 GGYTCGALAILLNEAEKVDLPFLIGVAFRO-GVECGFQGRTKKLVDCGYSFMOGAII 306
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 296 AFTQKLITIVDKLSSYSCKRPSGEDACTSSYGCTAKKSSANDYAKFGDFIQOSNQ 355
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 307 -----LPLRLRALHA-----OGDPALSMSHW----- 328
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 356 IGPFHNALQOYIILCSQVLEGLRDKPGKNDYHSCYCLGSLAVSQYSAMDTGSCP 415
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 329 ---MFHQALQDEYILMCCQCPAGGLDKPKSRDFYHTCYCLSGLSINQHG----SGAM 381
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 416 LPQHVLPYSNLEPIHPLVNVVLDKHTAYEFSSSE 452
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 382 LHDVVMGVPENVLPQTHPVYVIGDPKVIAQTHTFLQK 418
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```

RESULT 3
US-07-935-087-3
; Sequence 3, Application US/07935087
; Patent No. 6083917
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
```

```
APPLICANT: GOLDSTEIN, JOSEPH L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: THE IDENTIFICATION,
TITLE OF INVENTION: CHARACTERIZATION,
TITLE OF INVENTION: AND INHIBITION OF FARNESYL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESS: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1 (converted to ASCII-DOS)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/935,087
FILING DATE: 19920824
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/822,011
FILING DATE: 01/16/92
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:269/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-935-087-3

Query Match          39.1%; Score 942.5; DB 3; Length 437;
Best Local Similarity 43.1%; Pred. No. 2,8e-96;
Matches 197; Conservative 64; Mismatches 137; Indels 59; Gaps 7;
```

```
DB 329 ---MFHQALAEYILMCCQCPAGLLDPKPKSNDPHTYTCYCLSLAQHFG----SGAM 381
QY 416 LPQHVIGPYSNLEPIHPYLVNDKHTATVEFFSEE 452
DB 382 LHDVVGAVPENLQPTHEVNIQDPKVIOATTFHLOK 418

RESULT 4
PCT-US93-08062-3
Sequence 3, Application PC/TUS9308062
GENERAL INFORMATION:
APPLICANT:
SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.
SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.
SEQUENCE CHARACTERISTICS: REISS, YUVAL.
SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.
ADDRESS: THE IDENTIFICATION,
ADDRESS: CHARACTERIZATION AND
ADDRESS: INHIBITION OF
ADDRESS: FARNESYLTRANSFERASE
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESSES:
ADDRESS: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK/ASKII
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08062
FILING DATE: AUGUST 24, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/935,087
FILING DATE: 24 AUGUST 1992 (24.08.92)
NAME: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTPD377/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US93-08062-3

Query Match          39.1%; Score 942.5; DB 5; Length 437;
Best Local Similarity 43.1%; Pred. No. 2,8e-96;
Matches 197; Conservative 64; Mismatches 137; Indels 59; Gaps 7;
```

Db 129 FLELCSPDGGFGGCGPYHLAFTYAANALCTIGTEAYVYINREKLLQVLSLKOPD 188
QY 177 GAFRHHDCGEIDVASTAIVASLVNILDFTKLAKGVGYIARCOTYEGGJAGEPYAEAH 236
Db 189 GSFLLHVGGEVDVSAVCAASVASTNITPDLFEGTAEMIRACOMWEGGICGVCMKAH 248
QY 237 GGYTCGGLAAILILNEAEKVDLPGLGWAFRO-GVECGPGRNTKLVDCGYSFWQGAII 295
Db 249 GGYTCGGLAAILILNEAEKVDLPGLGWAFRO-GVECGPGRNTKLVDCGYSFWQGAII 306
QY 296 AFTQRLITIVDKKSSYSCRPSEGEDACSTSYGCTAKSSAVDYAKFGDFIQGSNQ 355
Db 307 -----LPLRLRALHA-----OGDPALSMSH----- 328
QY 356 IGPLFPHNIALOOYITILCSQVLEGLRDGPKGNRDHYHSCYCLSGLAVSQYAMTDTGSCP 415
Db 329 ---MFOQALOEYILMCCQCPAGGLDPRKSDPYHTCYCLSLIAOHFC-----SGAM 381
QY 416 LPQHVLPYSNLEPIHPLVNVLDKHTAYEFESSE 452
Db 382 LHDVVLGVPEVNALQPTHPVYNIQPKVIAQTYFLQK 418

RESULT 5
US-08-424-268-10
Sequence 10, Application US/08424268
Patent No. 5821118
GENERAL INFORMATION:
APPLICANT: Omer, Charles A
APPLICANT: Diehl, Ronald E
APPLICANT: Gibbs, Jackson B
APPLICANT: Kohl, Nancy E
TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Power Mac
OPERATING SYSTEM: System 7.5.3
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,268
FILING DATE: 4/24/95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mulhard, David A
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18858PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
US-08-424-268-10

Query Match 39.08; Score 940.5; DB 2; Length 437;
Best Local Similarity 43.18; Pred. No. 4.7e-96;
Matches 197; Conservative 62; Mismatches 139; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAAAAADPLPR-----LTVQVEOMKVEARVCDIYRSLFGAAPTNRKS 56
Db 12 PRSSSPVNSSEPLSLRPEHARERLQDDSVETVSTIOAKVEERIOEVSST---KFNHLV 68
QY 57 IMLELRDQHIETVLPGLRHMGPAFHVLDANRPMILCYMWHPALILDEALDDLENDIID 116
Db 69 PRLVQREKHNHYLKRGRQLTDAYECLDASRPMILCYMILHLELLEIDEPQIVATDVQC 128
QY 117 FLARQDDKGVSGSGPGLPHIATTYAAVNTLVITGSEBALSSIRGNLYNPMLOMKVVS 176
Db 129 FLELCSPDGGFGGCGPYHLAFTYAANALCTIGTEAYVYINREKLLQVLSLKOPD 188
QY 177 GAFRHHDCGEIDVASTAIVASLVNILDFTKLAKGVGYIARCOTYEGGJAGEPYAEAH 236
Db 189 GSFLLHVGGEVDVSAVCAASVASTNITPDLFEGTAEMIRACOMWEGGICGVCMKAH 248
QY 237 GGYTCGGLAAILILNEAEKVDLPGLGWAFRO-GVECGPGRNTKLVDCGYSFWQGAII 295
Db 249 GGYTCGGLAAILILNEAEKVDLPGLGWAFRO-GVECGPGRNTKLVDCGYSFWQGAII 306
QY 296 AFTQRLITIVDKKSSYSCRPSEGEDACSTSYGCTAKSSAVDYAKFGDFIQGSNQ 355
Db 307 -----LPLRLRALHA-----OGDPALSMSH----- 328
QY 356 IGPLFPHNIALOOYITILCSQVLEGLRDGPKGNRDHYHSCYCLSGLAVSQYAMTDTGSCP 415
Db 329 ---MFOQALOEYILMCCQCPAGGLDPRKSDPYHTCYCLSLIAOHFC-----SGAM 381
QY 416 LPQHVLPYSNLEPIHPLVNVLDKHTAYEFESSE 452
Db 382 LHDVVLGVPEVNALQPTHPVYNIQPKVIAQTYFLQK 418

RESULT 6
PCF-US93-10442-10
Sequence 10, Application PC/TUS9310442
GENERAL INFORMATION:
APPLICANT: Omer, Charles A
APPLICANT: Diehl, Ronald E
APPLICANT: Gibbs, Jackson B
APPLICANT: Kohl, Nancy E
TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCF/US93/10442
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/968,782
FILING DATE: 10/30/92
ATTORNEY/AGENT INFORMATION:
NAME: Mulhard, David A
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18858
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid


```
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEITICAL: NO
FRAGMENT TYPE: N-terminal
PCT-US93-10442-10

Query Match
Best Local Similarity 43.1%; Score 940.5; DB 5; Length 437;
Matches 197; Conservative 62; Mismatches 139; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAAADPDLR-----LTVQVQMKVEARVGDITRSLFGAAPNTKS 56
DB 12 PSSSPVWSEPLYSLRREHARERLQDDSVETVTSIDAVKEKIEVSSY---KFNHLV 68
QY 57 IMLELRDQHIEYLTPGLRHNGPAFHVLDANRPMLCYMMVHPLALDEALDDLENDIID 116
DB 69 PRLVQGRKHNYHLKRGRLQTDAYECLDASRPMCLCYWILHSLDELDEPIQIVATDVCQ 128
QY 117 FLARQDKDGGSGGPGGOLPHLATTYAANTLVLTISEPALSSINRGNTYNFMLOMKYVS 176
DB 129 FLELQSPGGGPGGPGGYPHLAPTYAANALCTIGTEBYADIDINNEKLLQTLVSLKOPD 188
QY 177 GAFRHHGGEIDVASYTAISVASLVNILDKFLAKGVGYIARCQTEYEGGIGEPYABAH 236
DB 189 GSFLMHVGEVDVSAVCASVASLTNIITPDLFEETAMIRACQWMEGGIGVPGMEAH 248
QY 237 GGYTCGGLAAILLNEAEKVDLPGLIGVAFRO-GVECGFGRNKLVDGCVSFMQAGAI 295
DB 249 GGYTCGGLAAILVILKRESLNLSLLOWVTSROMREGGFQGRCKLVDCGCSFMQAG-- 306
QY 296 AFTOKLITIVDKLKSYSCKRPSGEDACSTSSYGCTAKSSAVDAYAKFGDFIOGSNQ 355
DB 307 -----LPLHLRALHA-----QGDPALSMSHM----- 328
QY 356 IGPLFHNALDQYITLCSQVLEGLRDKPCKNRNDHYSYCLSGLAVSQYSAMTDGSCP 415
DB 329 ---MHQOALQEVILMCCQCPAGGLDLPKSRDFFHTCYCLSGLSIAOHFG----SGAM 381
QY 416 LPOHVLGPGYSNLEPIHPLVNVVLDKYHTAYEFPSEE 452
DB 382 LHDVVLGVPENALQPTHVYVNIIGDPKVIQATYTFLOK 418

RESULT 7
US-08-424-268-20
Sequence 20, Application US/08424268
Patent No. 5821118
GENERAL INFORMATION:
APPLICANT: Omer, Charles A
APPLICANT: Diehl, Ronald E
APPLICANT: Gibbs, Jackson B
APPLICANT: Kohl, Nancy E
TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
TRANSFERASE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Power Mac
OPERATING SYSTEM: System 7.5.3
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424, 268
FILING DATE: 4/24/95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
```

```
NAME: Muthard, David A
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18858PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 819 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEITICAL: NO
FRAGMENT TYPE: N-terminal
US-08-424-268-20

Query Match
Best Local Similarity 43.1%; Score 940.5; DB 2; Length 819;
Matches 197; Conservative 62; Mismatches 139; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAAADPDLR-----LTVQVQMKVEARVGDITRSLFGAAPNTKS 56
DB 12 PSSSPVWSEPLYSLRREHARERLQDDSVETVTSIDAVKEKIEVSSY---KFNHLV 68
QY 57 IMLELRDQHIEYLTPGLRHNGPAFHVLDANRPMLCYMMVHPLALDEALDDLENDIID 116
DB 69 PRLVQGRKHNYHLKRGRLQTDAYECLDASRPMCLCYWILHSLDELDEPIQIVATDVCQ 128
QY 117 FLARQDKDGGSGGPGGOLPHLATTYAANTLVLTISEPALSSINRGNTYNFMLOMKYVS 176
DB 129 FLELQSPGGGPGGPGGYPHLAPTYAANALCTIGTEBYADIDINNEKLLQTLVSLKOPD 188
QY 177 GAFRHHGGEIDVASYTAISVASLVNILDKFLAKGVGYIARCQTEYEGGIGEPYABAH 236
DB 189 GSFLMHVGEVDVSAVCASVASLTNIITPDLFEETAMIRACQWMEGGIGVPGMEAH 248
QY 237 GGYTCGGLAAILLNEAEKVDLPGLIGVAFRO-GVECGFGRNKLVDGCVSFMQAGAI 295
DB 249 GGYTCGGLAAILVILKRESLNLSLLOWVTSROMREGGFQGRCKLVDCGCSFMQAG-- 306
QY 296 AFTOKLITIVDKLKSYSCKRPSGEDACSTSSYGCTAKSSAVDAYAKFGDFIOGSNQ 355
DB 307 -----LPLHLRALHA-----QGDPALSMSHM----- 328
QY 356 IGPLFHNALDQYITLCSQVLEGLRDKPCKNRNDHYSYCLSGLAVSQYSAMTDGSCP 415
DB 329 ---MHQOALQEVILMCCQCPAGGLDLPKSRDFFHTCYCLSGLSIAOHFG----SGAM 381
QY 416 LPOHVLGPGYSNLEPIHPLVNVVLDKYHTAYEFPSEE 452
DB 382 LHDVVLGVPENALQPTHVYVNIIGDPKVIQATYTFLOK 418

RESULT 8
PCT-US93-10442-20
Sequence 20, Application PC/TUS9310442
GENERAL INFORMATION:
APPLICANT: Omer, Charles A
APPLICANT: Diehl, Ronald E
APPLICANT: Gibbs, Jackson B
APPLICANT: Kohl, Nancy E
TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
TRANSFERASE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065-0907
COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10442
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/968,782
FILING DATE: 10/30/92
ATTORNEY/AGENT INFORMATION:
NAME: Mulharg, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18858
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 819 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
PCT-US93-10442-20

Query Match 39.0%; Score 940.5; DB 5; Length 819;
Best Local Similarity 43.1%; Pred. No. 1.3e-95;
Matches 197; Conservative 62; Mismatches 139; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAAADPLPR-----LTVQVEQMKVEAVGDIYSLFGAAPNPKS 56
DB 12 PSSSPVMESEPLYSRPHARELRQDDSVETVISIQAVEKEIGEVSSY---KFNILY 68
QY 57 INLELMROOHLEIYLPGRHMGPAFHYLDANRPWLCYWHYPLALLDELDDLENDIID 116
DB 69 PRLVLDREKHRYLKRGRQLTDAYECUDASRPWLCYWHLSLELDEPTIQWATDVCO 128
QY 117 FLARCODXGCGSGGPGQLPHLATTVAAVNTLVTTGSEFALSSINGNLVFMLOMKDVS 176
DB 129 FLELCOSPEGCGGPGQYPLHAPTYAANALCIGTEEAYDIINREKLLQYLSLKOPD 188
QY 177 GAFRMHDDGEIDVRSAYATISVAVSNILDFKLAKGVGYIARCOTYEGGIAGEPYAAH 236
DB 189 GSFLMHDDGEVDVRSAYATISVAVSNILDFKLAKGVGYIARCOTYEGGIAGEPYAAH 248
QY 237 GGYTCGGLAALILNEAKVDLPGLIGVAFRO-GVECGFGRTNKLVDGYSFWOGAAI 295
DB 249 GGYTCGGLAALILNEAKVDLPGLIGVAFRO-GVECGFGRTNKLVDGYSFWOGAAI 306
QY 296 AFTOKLITIVYKOLKSSYSCRRPSGDEACSTSSYCGTAKKSSAVDYAKFGDFIQOSNQ 355
DB 307 -----LPLRLHRAALHA-----QGDPALSMRHW----- 328
QY 356 IGPLPHNTALDOYITLLGSOVLEGLRDKPKGNRDHYSCYCLSLAVSOYSAMTDGSCP 415
DB 329 ---MFHQALOEYILMCOCPAGGLLDKPKGSRDYHTCYCLSLAIOHFG---SGAM 381
QY 416 LPOHVLGPRYSNLLEPIRLYVNVLDKYNHTAYEFSSE 452
DB 382 LHDVVLGVPENALQPTHEPVYNIQPKVYQATYTFLOK 418

RESULT 9
US-08-424-268-6
Sequence 6, Application US/08424268
Patent No. 5821118
GENERAL INFORMATION:
APPLICANT: Omer, Charles A
APPLICANT: Diehl, Ronald E
APPLICANT: Gibbs, Jackson B

APPLICANT: Kohl, Nancy E
TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
TRANSFERASE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Power Mac
OPERATING SYSTEM: System 7.5.3
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,268
FILING DATE: 4/24/95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mulharg, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18858PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
US-08-424-268-6

Query Match 39.0%; Score 939.5; DB 2; Length 437;
Best Local Similarity 43.1%; Pred. No. 6e-96;
Matches 197; Conservative 62; Mismatches 139; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAAADPLPR-----LTVQVEQMKVEAVGDIYSLFGAAPNPKS 56
DB 12 PSSSPVMESEPLYSRPHARELRQDDSVETVISIQAVEKEIGEVSSY---KFNILY 68
QY 57 INLELMROOHLEIYLPGRHMGPAFHYLDANRPWLCYWHYPLALLDELDDLENDIID 116
DB 69 PRLVLDREKHRYLKRGRQLTDAYECUDASRPWLCYWHLSLELDEPTIQWATDVCO 128
QY 117 FLARCODXGCGSGGPGQLPHLATTVAAVNTLVTTGSEFALSSINGNLVFMLOMKDVS 176
DB 129 FLELCOSPEGCGGPGQYPLHAPTYAANALCIGTEEAYDIINREKLLQYLSLKOPD 188
QY 177 GAFRMHDDGEIDVRSAYATISVAVSNILDFKLAKGVGYIARCOTYEGGIAGEPYAAH 236
DB 189 GSFLMHDDGEVDVRSAYATISVAVSNILDFKLAKGVGYIARCOTYEGGIAGEPYAAH 248
QY 237 GGYTCGGLAALILNEAKVDLPGLIGVAFRO-GVECGFGRTNKLVDGYSFWOGAAI 295
DB 249 GGYTCGGLAALILNEAKVDLPGLIGVAFRO-GVECGFGRTNKLVDGYSFWOGAAI 306
QY 296 AFTOKLITIVYKOLKSSYSCRRPSGDEACSTSSYCGTAKKSSAVDYAKFGDFIQOSNQ 355
DB 307 -----LPLRLHRAALHA-----QGDPALSMRHW----- 328
QY 356 IGPLPHNTALDOYITLLGSOVLEGLRDKPKGNRDHYSCYCLSLAVSOYSAMTDGSCP 415
DB 329 ---MFHQALOEYILMCOCPAGGLLDKPKGSRDYHTCYCLSLAIOHFG---SGAM 381
QY 416 LPOHVLGPRYSNLLEPIRLYVNVLDKYNHTAYEFSSE 452
DB 382 LHDVVLGVPENALQPTHEPVYNIQPKVYQATYTFLOK 418

RESULT 10
PCUS93-10442-6
Sequence 6, Application PC/TUS9310442
GENERAL INFORMATION:
APPLICANT: Omer, Charles A
APPLICANT: Diehl, Ronald E
APPLICANT: Gibbs, Jackson B
APPLICANT: Kohl, Nancy E
TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
TRANSFERASE
TITLE OF INVENTION: Transferase
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10442
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/968,782
FILING DATE: 10/30/92
ATTORNEY/AGENT INFORMATION:
NAME: Mulnard, David A
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18858
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
PCUS93-10442-6

Query Match 39.0%; Score 939.5; DB 5; Length 437;
Best Local Similarity 43.1%; Pred. No. 6e-96;
Matches 197; Conservative 62; Mismatches 139; Indels 59; Gaps 7;

5 POSTPTGDDPAADPLPR-----LTVTQVEOMKVEARVGDVYSLFGAAPTAKS 56
12 PSSSPVWSEPLYSRPHARERLQDDSVETVSIQAKVEERIQVFSY---KFNHLV 68
57 INLELMRQHOIEYLTPLGRHNGPAFHVLDANRPMWCYWWHPALALIDEALDDLENDIID 116
69 PRLVLRQREKHRYLKRGLTDLAYECLDASRPMLCYWILHSHLELDEPIQIVATDVQCQ 128

117 FLARCODKDGSGGPGQLPLATTYAANTLVLTIGSERALSSINGNLNPMLOMKDVS 176
129 FLELCQSPGEGFGGPGQYPLLATYAAVNAALCIIGTEERYDVINERKLIQVLSIKQPD 188
177 GAFRNHGDGEIDVRASTAYASVAVNIIDFKIAGVGYIARCOTYEGGIAGEPYAEAH 236
189 GSFIMHNDGEVDVAVSACASVASTLTITPDLFEQTAETIARCOQWMEGIGVYGEAEAH 248
237 GGYTFCGTAALILINAEKVDLPGLIGVAFRO-GVECGFGRTNKLNVGCVSFGOGAAI 295
249 GGYTFCGTAALILINAEKVDLPGLIGVAFRO-GVECGFGRTNKLNVGCVSFGOGAAI 306
296 AFTQKLTIVDKQKSSYSCKRPSGEDACSTSSYGGCTAKSSANDYAKFGFDITQOSNQ 355

DB 307 -----LPLLRALHA-----OGDPLSMSRW----- 328

QY 356 IGPLEFHNALAOXYITLCSQVLEGLRDKRCKNBDHYHSCYCLGIAVSOYAMPTGSCP 415
DB 329 ---MFHQQLQLEYILMCCQPTGLLQKPKSRPFYHTCYLSGLSIAOHFG-----SGAM 381

QY 416 LPQHVLGPSNLEPIHPLVNVVLDKRYHTAYEEFSEB 452
DB 382 LHDVVLGVENALQPTHRVYVNIQPDVYQATMFLQK 418

RESULT 11
US-07-935-087-7
Sequence 7, Application US/07935087
Patent No. 6083917
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
IDENTIFICATION OF
TITLE OF INVENTION: THE IDENTIFICATION,
CHARACTERIZATION, AND INHIBITION OF FARNESYL
TRANSFERASE
TITLE OF INVENTION: PROTEIN TRANSFERASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: IBM PC COMPATIBLE
SOFTWARE: WORDPERFECT 5.1 (converted to ASCII-DOS)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/935,087
FILING DATE: 19920824
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/822,011
FILING DATE: 01/16/92
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: US/07/822,011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-935-087-7

Query Match 38.6%; Score 931.5; DB 3; Length 444;
Best Local Similarity 42.7%; Pred. No. 4.8e-95;
Matches 195; Conservative 62; Mismatches 141; Indels 59; Gaps 7;

5 POSTPTGDDPAADPLPR-----LTVTQVEOMKVEARVGDVYSLFGAAPTAKS 56
12 PSSSPVWSEPLYSRPHARERLQDDSVETVSIQAKVEERIQVFSY---KFNHLV 68
57 INLELMRQHOIEYLTPLGRHNGPAFHVLDANRPMWCYWWHPALALIDEALDDLENDIID 116
69 PRLVLRQREKHRYLKRGLTDLAYECLDASRPMLCYWILHSHLELDEPIQIVATDVQCQ 128
117 FLARCODKDGSGGPGQLPLATTYAANTLVLTIGSERALSSINGNLNPMLOMKDVS 176

FLING DATE: ABANDONED
CLASSIFICATION: 435
APPLICATION NUMBER: PCT/US/91/02650
FLING DATE: 18-APR-1991
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/615,715
FLING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/510,706
FLING DATE: 18-APR-1990 (ABANDONED)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:432/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-429-964-7

Query Match 37.3%; Score 898.5; DB 2; Length 387;

Best Local Similarity 44.3%; Pred. No. 1.8e-91;
Matches 185; Conservative 58; Mismatches 124; Indels 51; Gaps 6;

36 YEARYGDIYRSLFGAAPTSTKSMLEMRDQHIETLPGRLHMGPAFHYLDANRPMICYWM 95
1 VEEKIOEVFSSY---KFNHLVPRVLVLOREKHFIYLRGLRLDLDAYECIDASRPMLCYWI 57
56 VHPALDLDEALDDLENDIIDFLARCODKDGYSGGPGQLPHLATTYAAVNTLVITGSR 155
58 LHSLELDEPIPOIVATDVCOFLCOSPFGCGGPGQYPHLATPYAAVNALCTITGEE 117
156 ALSSINRGNLYNFMLOKMDVSGAFRMDGGEIDVRSATYASIVNLIDFKLAKGVD 215
118 AYDIINRKLQVLYSLQPDGSLMHVGEVDVRSAYCAASVASTLNTIITPDLEGTAE 177
216 YIARQTYEGGIAGEPYAEAHGTYTFCGLAALILNEARKVDIPLIGVAFRQGV-BCG 274
178 WIARQNMGGIGIGVPGMEAHGTYTFCGLAALVILKRESLNKSLQVTSRQMLFEGG 237
275 FQGRTNKLYVDCYISFWOGAALAFQKLTIVDKOLKSSYSCKRPSGEDACSTSSYGTAK 334
238 FQGRCNKLYVDCYISFWOGA-----LLPLHLRALHA-----QDDPALSMHW----- 278
335 KSSSAVDYAKFGFPIQDSNGIGPLFNIALQOYIILCSQVLEGGILRDKPGKRNDRHYSC 394
279 -----MFHQALQOYIILMCCQCPAGGILDPGSRDPFYHTC 314
395 YCLSLAVSOTYSAWTDGSCPLDQHVLPYSLNLEPIHPLVNVLDKYHTAVFEFSEE 452
315 YCLSLSTIAQHFQ-----SGAMLHGVYLVGPEVNALQPTHHVYINIGPKYVQATTTFLQK 368

RESULT 14

PCT-US93-08062-7

Sequence 7, Application PC/TUS9308062

GENERAL INFORMATION:

APPLICANT:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.

SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.

SEQUENCE CHARACTERISTICS: REISS, YUVAL

SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.

ADDRESS: METHODS AND COMPOSITIONS FOR

ADDRESS: THE IDENTIFICATION,

ADDRESS: CHARACTERIZATION AND

ADDRESSEE: INHIBITION OF
ADDRESSEE: FARNESYLTRANSFERASE
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK/ASKII
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08062
FLING DATE: AUGUST 24, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/935,087
FLING DATE: 24 AUGUST 1992 (24.08.92)
NAME: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTFD377PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US93-08062-7

Query Match 37.3%; Score 898.5; DB 5; Length 387;

Best Local Similarity 44.3%; Pred. No. 1.8e-91;
Matches 185; Conservative 58; Mismatches 124; Indels 51; Gaps 6;

36 YEARYGDIYRSLFGAAPTSTKSMLEMRDQHIETLPGRLHMGPAFHYLDANRPMICYWM 95
1 VEEKIOEVFSSY---KFNHLVPRVLVLOREKHFIYLRGLRLDLDAYECIDASRPMLCYWI 57
56 VHPALDLDEALDDLENDIIDFLARCODKDGYSGGPGQLPHLATTYAAVNTLVITGSR 155
58 LHSLELDEPIPOIVATDVCOFLCOSPFGCGGPGQYPHLATPYAAVNALCTITGEE 117
156 ALSSINRGNLYNFMLOKMDVSGAFRMDGGEIDVRSATYASIVNLIDFKLAKGVD 215
118 AYDIINRKLQVLYSLQPDGSLMHVGEVDVRSAYCAASVASTLNTIITPDLEGTAE 177
216 YIARQTYEGGIAGEPYAEAHGTYTFCGLAALILNEARKVDIPLIGVAFRQGV-BCG 274
178 WIARQNMGGIGIGVPGMEAHGTYTFCGLAALVILKRESLNKSLQVTSRQMLFEGG 237
275 FQGRTNKLYVDCYISFWOGAALAFQKLTIVDKOLKSSYSCKRPSGEDACSTSSYGTAK 334
238 FQGRCNKLYVDCYISFWOGA-----LLPLHLRALHA-----QDDPALSMHW----- 278
335 KSSSAVDYAKFGFPIQDSNGIGPLFNIALQOYIILCSQVLEGGILRDKPGKRNDRHYSC 394
279 -----MFHQALQOYIILMCCQCPAGGILDPGSRDPFYHTC 314
395 YCLSLAVSOTYSAWTDGSCPLDQHVLPYSLNLEPIHPLVNVLDKYHTAVFEFSEE 452
315 YCLSLSTIAQHFQ-----SGAMLHGVYLVGPEVNALQPTHHVYINIGPKYVQATTTFLQK 368

RESULT 15

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2002, 17:58:05 ; Search time 39 seconds
(without alignments)
1113.651 Million cell updates/sec

Title: US-09-786-675-12

Perfect score: 2411

Sequence: 1 MDPSPGSPPTGDDPAAD.....PLYNVLDKHTAFEPFSEE 452

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*

1: PIR1:*\n2: PIR2:*\n3: PIR3:*\n4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length DB	ID	Description
1	1357.5	56.3	470	2 T07673	farne syltranstrans
2	1353.5	56.1	470	2 T07605	protein farne syltr
3	1315.5	54.6	419	2 J02354	farne syl-diphospha
4	942.5	39.1	437	2 A40037	protein farne syltr
5	940.5	39.0	437	2 B49274	protein farne syltr
6	935.5	39.0	437	2 C49274	protein farne syltr
7	805.5	33.4	401	2 T21291	hypothetical prote
8	623.5	25.9	382	2 T37836	probable protein f
9	618.5	25.7	431	1 BVBYPD	probable protein p
10	342.5	14.2	375	2 T00565	geranylgeranyl-dip
11	327.5	13.6	311	2 S65091	geranylgeranyltran
12	326	13.5	325	2 S59834	geranylgeranyltran
13	320	13.3	377	2 AS3044	probable protein p
14	313	13.0	377	2 B53044	geranylgeranyl-dip
15	297.5	12.3	325	2 T15296	hypothetical prote
16	289.5	12.0	355	2 S41866	geranylgeranyltran
17	282	11.7	331	2 B45977	Rab geranylgeranyl
18	279	11.6	331	2 G02431	geranylgeranyl tra
19	278	11.5	339	2 JC6177	geranylgeranyl-dip
20	275.5	11.4	304	2 I49116	hypothetical prote
21	244.5	10.1	360	2 T27022	hypothetical prote
22	190.5	7.9	376	1 RGRY43	cell division cont
23	97	4.0	1090	1 S11823	alpha-dextrin endo
24	96.5	4.0	2703	1 A24420	notch protein - fr
25	95.5	3.9	705	2 A41322	N-acetylneuramoyl-L
26	93.5	3.9	2512	2 E70751	hypothetical prote
27	92.5	3.8	346	2 A70590	hypothetical prote
28	91.5	3.8	791	2 T42691	hypothetical prote
29	90.5	3.8	271	2 F69442	hypothetical prote

30	90	3.7	343	1 RGRBP1	recombinase - phag
31	90	3.7	350	2 JC7213	Cre recombinase pr
32	90	3.7	608	2 T34594	probable long-chain
33	90	3.7	1039	2 C84745	hypothetical prote
34	89.5	3.7	2895	2 H85362	hypothetical prote
35	89.5	3.7	334	2 A58195	cathepsin L (EC 3.
36	89.5	3.7	704	2 T03478	probable DNA-direc
37	89.5	3.7	1025	2 T45647	receptor protein k
38	89	3.7	312	2 E71624	reflin PRB0055c - m
39	89	3.7	1436	2 T14895	DNA helicase 1 - A
40	88.5	3.7	2155	2 T30197	alpha tectorin - m
41	88	3.6	281	2 G87451	hypothetical prote
42	88	3.6	161	2 G89916	hypothetical prote
43	88	3.6	1214	2 G70953	probable such prot
44	87.5	3.6	404	2 A84211	hypothetical prote
45	87.5	3.6	765	2 H84247	adaptive-response

ALIGNMENTS

RESULT 1	
T07673	farne syltranstransferase (EC 2.5.1.29) chain B - tomato
C:Species: Lycopersicon esculentum (tomato)	
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-May-2000	
C:Accession: T07673	
R:Ratovsky, S.; Trueblood, C.E.; Callen, K.L.; Naitza, J.O.; Jenkins, S.M.; Rine, J.; Mol. Cell. Biol. 17, 1986-1994, 1997	
A:Title: Plant farne syltransferase can restore yeast ras signaling and mating.	
A:Reference number: 207721; MUID:97219988	
A:Accession: T07673	
A>Status: Preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1-470 <YAL>	
A:Cross-references: EMBL:U83708; NID:q1815667; PIDDN:ANAC49666.1; PTD:q1815668	
A:Experimental source: cultivar VENT Cherry LA1221	
A>Note: farne sylates proteins	
C:Genetics:	
A:Gene: FTB	
C:Superfamily: DPRI protein	
C:Keywords: heterodimer; transferase	
Query Match	56.3%; Score 1357.5; DB 2; Length 470;
Best local similarity	57.3%; Pred. No. 4.8e-108;
Matches 256; Conservative 68; Mismatches 100; Indels 23; Gaps 3;	
QY 25 RLTVTQVEQMKYEAARVDIYRSLEGAAPNTKSIIMLEWRDQITEVLTPLRMNGPAHYVL 84	
DB 5 KYKTLLEDQWVERREIYDFYISPNPSDLITERDKHKGYSOGILRKIGSFYVL 64	
QY 85 DANRPMVLKVMWHPALALDEALDDLENDIIDFLARCQDKGSGGPGOLPHLATTYAA 144	
DB 65 DMSRPMVLKWTLSIALLGESIGKLENDALDPLTRQDDGGSGGPGOMHLATTYAA 124	
QY 145 VNPVTITGSERALSSINGNLINFMLOKDVSGAFRMDHGGELIDVPASTAIASVSLNI 204	
DB 125 VNSLTTLKPEALSSINREKLYLPLLRKDAISGCFRMDHGGEDVACRTAISVANITLT 184	
QY 205 LDFPLAKGQGVFIARCYEGGIAEGEPAEABHAGYFGCGLAALILNLEAKEDLSLIGW 264	
DB 185 VDDELLHGVGNVILSCQYTBEGGINGEPGSEAHGYTCGLAAILINVEDRDLGLIDW 244	
QY 265 VAPRGQVECGFGQGTNRKLVDCGYFMOGAALATFOKLITIVDKLKSYSYSCRRPGEDAC 324	
DB 245 VYFRQGVGEGFGQGTNRKLVDCGYFMOGAAYVFLORLNLIVHROLISNDLSTESADSS 304	
QY 325 ST-----SSY-----GCTAKKSSAVDYAKGFPFIOSONIGPLPHN 362	
DB 305 ESELDSEDEEHLEGISSHQDFFPLGQACAOENASHPKIADYGFETINRPLAMRPLDS 364	
QY 363 IALQGYILICQSVLEGGKRDKPGKRNDRHYSCTCLSGLAISYSAANTDTGSCPLDQHYLG 422	


```

Db      12 PSSSPWSEPLTSLRPEHARERLQDDSVETVTSIEQAKVEEKIOEYFSSY---KENHLY 68
QY      57 IMELMRDHOIEVLTFGRLRMGPAFHYLDANRPVLCYMMVPLALLDEALDDLEDDLEIID 116
Db      69 PRLVLOREKREHYTLKGLNQLTDATCELDASPMVLCWILHSELDDEPIPOIVARDVCO 128
QY      117 FLARCDKDGSGSGSGFQLPHLATTYAAVNTLVYIGSERALSSINRCNLNFMLOKDVYS 176
Db      129 FLELCOSPDGCFGSGGQGYPLAPTYAAVNALCIETGEAEAVNVINREKLLOYLYSLKOPD 188
QY      177 GAFRMDGGEIDRASYTAISVASLVNTLDFEKLKAGVDYARQOTEGGSIAGEPAEAEH 236
Db      189 GSEFMHVGGEVDKRSATCAASVASTLNTITPDLEEGTAEMTARCONNEGIGVGPOMEAH 248
QY      237 GGYTFPGALAILLNAEKVDPSLIGWVAERQ-GVECGFQGRNTKLVYDCSYSPWQAAI 295
Db      249 GGYTFPGALAILLNAEKVDPSLIGWVAERQ-GVECGFQGRNTKLVYDCSYSPWQAAI 306
QY      296 AFYQKLTLYDRQJLMSYSCKRPSGEDACSTSSVGYCTAKKSSAVDYAKGFDFIQOSNQ 355
Db      307 -----LRLPLHRLHRA-----QGDPLALSMSHW----- 328
QY      356 IGPLFNLIALOOYITLLCSOVLECGJLRDPRGNKRHDHYSCTGLSLAVSOYSAMTIDGSCP 415
Db      329 ---MFHQQAQAEVETILMCCGCPAGGLDKPGRSBDYHNYCYLSTGLSLAQHFG-----SGAM 381
QY      416 LPQHVLAGPYSNLLEPIHPLLYNVLNLDKYNHTAYEFSSE 452
Db      382 LHDVYMGVPEENVLQPTPHVYINIGPKRVIOATTHFLQK 418

```

RESULT 5
B49274
protein farnesyltransferase (EC 2.5.1.-) beta subunit - human
N:Alternate names: farnesyl-protein transferase beta subunit; FTase beta subunit; prenylase beta subunit; prenylase beta subunit; prenylase beta subunit; prenylase beta subunit
S:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C:Accession: B49274, I60951
R:Omer, C.A.; Kral, A.; Diehl, R.E.; Prendergast, G.C.; Powers, S.; Allen, C.M.; Gibbs
B:Biochemistry 32, 5167-5176, 1993
A:Title: Characterization of recombinant human farnesyl-protein transferase: cloning, ex
A:Reference number: A49274; MUID:93264431
A:Accession: B49274
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-437 <OME>
A:Experimental source: Placenta
A:Note: sequence extracted from NCB1 backbone (NCBI:132829)
R:Anders, D.A.; Miletovich, A.; Ozececi, T.; Wenzlau, J.M.; Brown, M.S.; Goldstein, J.L.
S:Genomics 18, 105-112, 1993
A:Title: cDNA cloning of the two subunits of human CAAX farnesyltransferase and chromoso
A:Reference number: A47659; MUID:94102736
A:Accession: I60951
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Residues: 51-282, 'L', 284-437 <RES>
A:Molecule type: mRNA
C:Cross-references: GB:LI0414; NID:g388757; PIDN:AAA80286.1; PID:g388758
C:Genetics:
A:Gene: GDB:FTTB
A:Cross-references: GDB:138174; OMIM:134636
A:Map position: 14q23-14q24
S:Superfamily: DPM protein
S:Keywords: transferase

```

Qy      5  POSTPPGDDPAAADBDLPR-----LIVTQVEQMKVEARNGDITRSLGCAAPITKS 56
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      12  PPSPPVMSVSLTSLRREARERLQDDSVETYSLEQAKVEEKIQEIDVSS--KFMHLY 68
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          Matches 197;  Conservative  62;  Mismatches 139;  Indels  59;  Gaps  7

Query Match      39.0%;  Score 940.5;  DB 2;  Length 457;
Best Local Similarity 43.1%;  Pcore No. 2e-72;

```

```

QY 57 IMELMDOJIEULTFGLRHMGPFAHVUDARPMICWYHNPALDEADDDLENDIID 116
Db 69 PRVLQREKHFHYLTKRGRLQJLTDAYECLDASRPMICWYHLSJELLEDEPIQIVANDVQC 128
QY 117 FLARCODKOGYSGGSGCOLPHLATYVAVNVTLYTISEBRLLSSNGNLXNFMLOKQDVS 176
Db 129 FLELCOSPEBGFGGGQPHLATYVAVNMLCTIGTEAEVDIINREKLYQYLSIKQPD 188
QY 177 GAFPMHGGSEIDVRASYTAISVASLVNITLDEFLAKGVGDYIARCOYEGGIAGEAPEAH 236
Db 189 GSEFLMHVGGSEVDYRSAYCAASVASLTNITPDELFEGTAEMIAROMNEGGIGGVPEMEEH 248
QY 237 GGYVFCGLALILNBAEKVDPSLIGWVAERO-GVECGFGQFGRNKLVDGCSFWMGAI 295
Db 249 GGYTFGCALALVILKREBSLNLSLQWYTSRQHRFEGGFGQGRNKLVDGCSFWMG-- 306
QY 296 AFYOKLITTYDKOLAKSYSCRRPSEGDACSTSYGCTAKKSSAVDYAKGFDFIOOSNO 355
Db 307 ----LPLLRHLRHLA-----GGDPALSMSHW----- 328
QY 356 IGPLFENALIQYLTILCSQVLEGLGRDRPGKRNPDHYHSCYCLSGLAVSQYSANTDTGSCP 415
Db 329 ---MFHQOALQYETILMCCOCPPAGGLDKRGRSBDYHVCYCLSGLSIAQIFG---SGAM 381
QY 416 LPQHVUGPYSNLEPFIHPLXNVVLDKYHTAEEFSEE 452
Db 382 LHDVUGLGPENALQPHYVYVINGPDKVIAQATTFYQK 418

```

RESULT 6
C49274
protein farnesyltransferase (EC 2.5.1.-) beta subunit - bovine
N|alternates names: farnesyl-protein transferase beta subunit; FPPase beta subunit; pr
C|species: Bos primigenius taurus (cattle)
C|date: 25-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999
C|accession: C49274
R|omer, C.A.; Kiral, A.M.; Diehl, R.E.; Prendergast, G.C.; Powers, S.; Allen, C.M.; Gl
Biochimica 32, 5167-5176, 1993
A|title: Characterization of recombinant human farnesyl-protein transferase: cloning;
A|reference number: A49274; MUID:93264431
A|accession: C49274
A|status: preliminary; not compared with conceptual translation
A|molecule type: mRNA
A|residues: 1437 <OMP>
A|experimental source: brain
A|note: sequence extracted from NCBI backbone (NCBIP:132834)
C|superfamily: DPL1 protein
C|keywords: transferase

[illegible]

A:Accession: T37741
A:Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: DNA
A:Residues: 1-311 <PRE>
A:Cross-references: EMBL:A035248; PIDB:CAA22847.1; GSPDB:GND0066; SPDB:SPAC167.02
A:Experimental source: strain 97Zh-, cosmid C167
C:Genetics:
A:Gene: SPAC167.02
A:Map position: 1
A:Insertions: 18/3; 69/1; 108/1; 180/1; 224/3
C:Superfamily: DPrI protein

Query Match 13.6%; Score 327.5; DB: 2; Length 311;
Best Local Similarity 24.6%; Pred. No. 3.4e-20;
Matches 96; Conservative 61; Mismatches 139; Indels 95; Gaps 9;

OY 58 MLELMRDQHIETLTPLGRHMGPAFHYLDANRPWL-----CYMVPRLALDEALDD 109
Db 1 MAVLLRKKHLSY----IMDIGNTDELDF--WLRKHVSAIVYSQSMFWLLKKNQID 53
OY 110 LENDIIFGLRCODKQGCGGGOLPHATTTAAVNNTLVITSEBRASSINGNLXNPM 169
Db 54 KER-IYVFSLSCLESCEGFACFGHDHDTTNYAVQVLAMDLS---LHVVDKDKASST 109
OY 170 LOMKDVSAGAFRMHGDGEIDVRASYATAISVALVINLDEKLAKGVGYDIARCOYTEGGIG 229
Db 110 IGLNEGSGMKQWRMCEDIDARFLYSGINCLATILGDLTDLNKTAVDMLCMYNFDDGFG 169
OY 230 EPVAEANGCTFFGLMALILINEAEKVDP.LSICGVAPROGVECSFGGRTNKLYDCGSF 289
Db 170 CRGASHNGAWFTCVAAKTLINKLIDLDELLGMWISRKQKGGKLGSRPEKLPDSCTGH 229
OY 290 WOGAIAINFOTKLTITYDKOLKSSYSCKRRPSGEDACSTSYCTAKKSSAVDYAKRGPDF 349
Db 230 WDLSPLLAITIKRL-----DW 243
OY 350 IQGNOIQCPFEHNIALDOQYILLCSQYLEGRLDRPKRNDRHNSCYCLSGLAISOXSAMT 409
Db 244 IDRNQLT-----DFLGTQDNADSGCFADRKEADTYVHNCFSLAGLSILOF---- 289
OY 410 DTGSCPRLPQHVLGPYSMLERHPILYNVLD 440
Db 290 -----PN-----IEPVDPFRFCIPLE 304

RESULT 12
S59834
Probable protein prenilyltransferase (EC 2.5.1.-) Bcr2 - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: geranyl-geranyltransferase beta chain; protein P9705.12; protein YPRU
C:Species: *Saccharomyces cerevisiae*
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 26-Aug-1999
C:Accession: S59834; S22843; S15399; B32569; S07612
R:Pauley, A.
submitted to the EMBL Data Library, April 1995
A:Description: The sequence of *S. cerevisiae* cosmid 9705.
A:Reference number: S59829
A:Accession: S59834
A:Molecule type: DNA
A:Residues: 1-325 <PAD>
A:CROSS-references: EMBL:U25842; NID:g786312; PIDB:AAA68110.1; PID:g786324; MIPS:YPR176c
R:Peterson-Bjorn, S.; Harrington, T.R.; Friesen, J.D.
Yeast 6, 345-352, 1990
A>Title: An essential gene in *Saccharomyces cerevisiae* shares an upstream regulatory element
A:Reference number: S22843; MOID:90371957
A:Accession: S22843
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-21, 'N', 23-325 <PERT>
R:Rossi, G.; Jiang, Y.; Newman, A.P.; Ferro-Movick, S.
Nature 351, 158-161, 1991
A>Title: Dependence of Ypr1 and Sec2 membrane attachment on Bcr2.
A:Reference number: S15399; MOID:91232583
A:Accession: S15399

```

A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Structure type: DNA
A:Residues: 1-322 <MAT>
R:Peetersen B, Jørgen, S., Soltyk, A., Beggs, J.D., Friesen, J.D.
Mol. Cell. Biol. 9, 3638-3709, 1989
A:Title: PPP4 (RNA4) from Saccharomyces cerevisiae: Its gene product is associated w
A:Reference number: A93112; MUID:89384596
A:Accession: B32569
A:Molecule type: DNA
A:Residues: 1-21, 'N', 23-187 <PERT2>
A:Cross-references: GB:126597; NID:g172282; PIDN:AAA79331.1; PID:g800847
C:Genetics:
A:Gene: SCD:BET2
A:Cross-references: SCD:SC006380; MIPS:YPR176C
A:Map position: 16R
C:Superfamily: DPR1 protein
C:Keywords: transferase

Query Match          13.5%; Score 326; DB 2; Length 325;
Best Local Similarity 25.4%; Pred. No. 4,8e-20;
Matches 102; Conservative 61; Mismatches 118; Indels 120; Gaps 14;

OY      59  LEIMRDQHEIYLTPLGLRMGPAFHVLDANRP-----WL-----CYMWHPLALDELAL 106
Db       5  LTLLEKHIRYI-----ESLIDTKHNFEEWLTIELRLNGIYWGTLATCYLDSP-  52
          | : : : : : | : : : : : | : : : : : | : : : : : |
OY      107 DDDLENIIDFLARC-QDKDGYSGPGQLPHLNTTAAVNTLVT-----IGSER--AL 157
Db       53  ETYPKEEIVFVLTSCDDKDYGAFAFPFRHDHLLTTLISNVOIATIDALDYLGKRRKRL 112
          | : : : : : | : : : : : | : : : : : | : : : : : |
OY      158  SSIRGKLTLYFMLOKNDVSGAFRMDHGEIDVRASYTAISVASIVNIDFKLAKGVGYI  217
Db      113  ISIFRGN-----QLAD--GSFQGDREFGEVDTREVTYALSNLSIELTSEVAVDPAVDFV 164
          | : : : : : | : : : : : | : : : : : | : : : : : |
OY      218  ARCTYGGCIAGEPVAEAGHYTFEGLAALILNLEAKV---DLPSLIGVAFRQGVDECG  274
Db      165  LKCYNFDGGFGICLPNMESHAQAQFTCLGALAIANKLMLMSDDQLERIGMWLCEKRPFG  224
          | : : : : : | : : : : : | : : : : : | : : : : : |
OY      275  FQGTINKLVDCGCSFPGQAATAFTOKLITTYIDKQLKSSYCKRPSGEDACSTSSVGCTAK  334
Db      225  LMGPRSLPLPYCTSMWVLSLAIIGRL-----  251
          | : : : : : | : : : : : | : : : : : | : : : : : |
OY      335  KSSAVDYAKFGDFLQOOSNQICPLFNHIALQVYILLCSVLEGLGRDKPRKNRDHYHSC  394
Db      252  ---DWIKYK-----LTFELIKCQDEKKGQISDRPENVDFVHTV  288
          | : : : : : | : : : : : | : : : : : | : : : : : |
OY      395  YCLSGLVASQYSAMTDGSCPLRQHVLDGYPYNNLEPIHPLX  435
Db      289  FGVAIGLS-----LMGYDNLV-PIDPIY  309
          | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 13
A53044
geranylgeranyl-diphosphate geranylgeranyltransferase (EC 2.5.1.32) I beta chain - hum
C:Species: Homo sapiens (man)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24-Nov-1999
C:Accession: A53044
R:Zhang, F.L., Diehl, R.E.; Kohl, N.E.; Gibbs, J.B.; Giros, B.; Casey, P.J.; Omer, C.
J. Biol. Chem. 269, 3175-3180, 1994
A:Title: cDNA cloning and expression of rat and human protein geranylgeranyltransfera
A:Reference number: A53044; MUID:94148804
A:Accession: A53044
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-377 <ZHA>
A:Cross-references: GB:125441; NID:g466490; PIDN:AAA55888.1; PID:g466491
C:Genetics:
A:Gene: GDB:PGCT1B; GGTI: BGCI
A:Cross-references: GDB:305477
C:Superfamily: cell division control protein CDC43
C:Keywords: transferase

Query Match          13.3%; Score 320; DB 2; Length 377;

```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2002, 17:08:30 ; Search time 20 seconds

(without alignments)
875.062 Million cell updates/sec

Title: US-09-786-675-12

Perfect score: 2411
Sequence: 1 MDSPQSTPTPTGDDPAAMAD.....PLYNVVLDKYHTAYEFPSEE 452

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1315.5	54.6	419	1	PTTB_PEA
2	1155.5	47.9	404	1	PTTB_ARATH
3	944.5	39.2	437	1	PTTB_BOVIN
4	942.5	39.1	437	1	PTTB_RAT
5	940.5	39.0	437	1	PTTB_HUMAN
6	618.5	25.7	431	1	RAM1_YEAST
7	342.5	14.2	341	1	BET2_CANAL
8	327.5	13.6	311	1	PTB1_SCHPO
9	326	13.5	325	1	BET2_YEAST
10	320	13.3	377	1	PGT1_HUMAN
11	313	13.0	377	1	PGT1_RAT
12	297.5	12.3	325	1	PTTB_CAEEL
13	289.5	12.0	355	1	CMG2_SCHPO
14	282	11.7	331	1	PGTB_RAT
15	280	11.6	331	1	PGTB_HUMAN
16	278	11.5	339	1	PGTB_MOUSE
17	190.5	7.9	376	1	CAL1_YEAST
18	97	4.0	1090	1	PUL1_KLEPN
19	96.5	4.0	2703	1	NOTC_DROME
20	95.5	4.0	705	1	CEB1_BACSU
21	90	3.7	343	1	RECR_BP1
22	89.5	3.7	334	1	CATL_BOVIN
23	89.5	3.7	334	1	CATL_PIG
24	89.5	3.7	704	1	DP3E_RHOCA
25	89	3.7	679	1	TKT1_KIOLA
26	88	3.6	734	1	PURL_ZYMO
27	87	3.6	334	1	CATL_RAT
28	86.5	3.6	515	1	TRPE_BACSU
29	86.5	3.6	779	1	SNIL_MOUSE
30	86	3.6	368	1	PERO_LACSE
31	86	3.6	522	1	Y4LR_RHISM
32	86	3.6	759	1	CASI_ARATH
33	86	3.6	1298	1	ICP4_HSV11

34	85.5	3.5	998	1	LONH_PYRAB
35	85	3.5	1066	1	ITTA3_HUMAN
36	84.5	3.5	521	1	NIFK_AZOBR
37	84.5	3.5	702	1	LONH_HALNI
38	84.5	3.5	2832	1	NDVB_RHIME
39	84	3.5	334	1	CATL_MOUSE
40	84	3.5	684	1	FBL1_CHICK
41	84	3.5	5376	1	ZAN_MOUSE
42	83.5	3.5	986	1	GUN2_CLOSR
43	83	3.4	265	1	UBR1_RICPR
44	83	3.4	668	1	PAB5_ARATH
45	82.5	3.4	880	1	GUN4_THEFU

ALIGNMENTS

RESULT 1
ID PTTB_PEA STANDARD; PRT; 419 AA.
AC 004903:
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein farnesyltransferase beta subunit (EC 2.5.1.-) (CAAX
DE farnesyltransferase beta subunit) (RAS proteins prenyltransferase
DE beta) (Frase-beta).
GN PTTB.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxId=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ALASKA; TISSUE=Seedling;
RX MEDLINE=94105305; PubMed=8278509;
RA Yang Z., Cramer C.L., Watson J.C.;
RT "Protein farnesyltransferase in plants. Molecular cloning and
RT expression of a homolog of the beta subunit from the garden pea.";
RL Plant Physiol. 101:667-674(1993).
CC -1- FUNCTION: CATALYZES THE TRANSFER OF A FARNESYL MOIETY FROM
CC THE C-TERMINUS OF SEVERAL PROTEINS. THE BETA SUBUNIT IS
CC RESPONSIBLE FOR PEPTIDE-BINDING (BY SIMILARITY).
CC -1- CORRECTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
CC FAMILY.
CC -1- SIMILARITY: CONTAINS 5 PTTB REPEATS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L08664; AAA3649.1; -.
CC PIR: J02254; J02254.
CC DR HSP: Q02293; IFT1.
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; Prenyltrans; 5.
KW Transferase; Prenyltransferase; Repeat; Zinc.
FT REPEAT 68 109 PTTB 1.
FT REPEAT 119 160 PTTB 2.
FT REPEAT 167 208 PTTB 3.
FT REPEAT 215 256 PTTB 4.
FT REPEAT 329 371 PTTB 5.
FT METAL 241 241 ZINC (BY SIMILARITY).
FT METAL 243 243 ZINC (BY SIMILARITY).


```

Oy      301 T-----YINRMQL--VFDSLQQRVLVCLSLIPGGRNDKPRKRDFEYHICYL 348
Db      349 SGLSVAGHMLKDDEPTPLTRDIMGGSNLPEVOLLANTIMDYNEAIEFF 400

RESULT 3
PFTB_BOVIN ID PFTB_BOVIN STANDARD: PRT: 437 AA.
AC PA9355; O9T9S25;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein farnesyltransferase beta subunit (EC 2.5.1.-) (CAAX
DE farnesyltransferase beta subunit) (RAS proteins prenyltransferase
DE beta) (Frase-beta).
GN FNTB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain:
RX MEDLINE=93264431; PubMed=8494894;
RA Omer C.A., Karl A.M., Diehl R.E., Prendergast G.C., Powers S.,
RA Allen C.M., Gibbs J.B., Kohl N.E.;
RT Characterization of recombinant human farnesyl-protein transferase:
RT cloning, expression, farnesyl diphasic binding, and functional
RT homology with yeast prenyl-protein transferases."
RL Biochemistry 32:5167-5176(1993).
CC -1- FUNCTION: CATALYZES THE TRANSFER OF A FARNESYL MOIETY FROM
CC FARNESYL PYROPHOSPHATE TO A CYSTEINE AT THE FOURTH POSITION FROM
CC THE C-TERMINUS OF SEVERAL PROTEINS. THE BETA SUBUNIT IS
CC RESPONSIBLE FOR PEPTIDE-BINDING.
CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
CC FAMILY.
CC -1- SIMILARITY: CONTAINS 5 PFTB REPEATS.
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-ch).
CC CC
DR EMBL: L00633; AAA30524.1; -.
DR HSSP: Q02293; 1FP2.
DR InterPro: IPR001330; PrenylTrans.
KW Pfam: PF00432; prenyltans; 5.
KW Transferase; Prenyltransferase; Repeat; zinc.
FT REPEAT 123 164 PFTB 1.
FT REPEAT 174 215 PFTB 2.
FT REPEAT 222 263 PFTB 3.
FT REPEAT 270 312 PFTB 4.
FT REPEAT 332 374 PFTB 5.
FT METAL 287 ZINC (BY SIMILARITY).
FT METAL 299 ZINC (BY SIMILARITY).
FT METAL 362 ZINC (BY SIMILARITY).
SQ SEQUNCE 437 AA; 48767 MW; CE09DFA66AC6AB64 CRC64;

Query Match 39.2% Score 944.5; DB 1: Length 437;
Best Local Similarity 43.3%; Pred. No. 56-74;
Matches 188; Conservative 62; Mismatches 138; Indels 59; Gaps 7;
5 POSTSCRIPT PPAADDPDLPR-----LTFTGVGEAKKYEARGYDIYRSLFGCADNPKS 56

```

Dd	12	PPSSPTWSEPLYSLRPEHANEERLDQDSSVEFTVSTIQAKVEEKIQEVPSSY---KFNHLV	68
Qy	57	IMELMRDQHIEYLTPGLRHNHGRAPEHVLADNANRMCLCYWVHPLALLDLADLDDLENDIID	116
Dd	69	PRVLVIAQREKHNFHYLKRGLRQLTDAVECLDASRPMCLCYWILSHLELIDEPIDQMAVTVCO	128
Qy	117	FLARCDKKGSGYSGPGGLPHLATTVAAVTLVTIGSERALSSINRGVLNFMQLDMKDV	176
Dd	129	FLIELCGSPGGGFGGGPGGYPHLADPTVAAVNALCIIGTEEAAYDIVIREKLLQGLVLSQPD	188
Qy	177	GARMHMDGEIDVRSQYTAISVASTLVNIIIDPKLAKGVGYIARQCTYEGGIATAGERPYAEH	236
Dd	189	GSLTLMHDGGEVVRSAVCAASVASLTNIIIPDLFECTAEWILARCONWBGIGCVPGMEAH	248
Qy	237	GGYTFPGCALIILLNEAEKRVDPRLIGWVAFRQ-GVEGPGRGRTNKLVDGCTSPMOGAAI	295
Dd	249	GGYTFPGCALIYILKKERSLMLKSLQMWTSROMRREGGFGQGRCKNLVDGCTSPMOAG--	306
Qy	296	AFNQKLTITVDKQLSSYSCNRSPGECACSTSSGYCTAKKSSAVDYAKPFDPITQOSNQ	355
Dd	307	-----LLPLLRALMA-----QGDAIISMNR-----328	
Qy	356	IGLPEFNHIALQOYLILCSQVLEGGELRDKPGKNBDHYHSCYCLSGLAVSOYSAMTDTGSCP	415
Dd	329	---MFHQALQLEYIILMCQCPFGGLDKPKKSDPFYHCCTGLSLAQHFG---SGAM	381
Qy	416	LPQHVGPYSNLPEIHPHNVNVLDKHTHTYAEFFSE	452
Dd	382	LHDVYLCGPENNALQPTTHHYVYIIGDKYIAQTHTHFLQK	418

RESULT 4	
PFTB_RAT	
ID_PFTB_RAT	STANDARD: PRT; 437 AA.
AC	002293;
DT	01-APR-1993 (Rel. 25, Created)
DT	01-APR-1993 (Rel. 25, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Protein farnesyltransferase beta subunit (EC 2.5.1.-) (CMAX
DE	farnesyltransferase beta subunit) (RAS proteins prenylttransferase
DE	beta) (PTase-beta) .
GN	FMTB.
OS	Rattus norvegicus (Rat) .
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC	TISSUE=Brain;
RX	MEDLINE=91309145; PubMed=1855253;
RT	Chen W.-J., Andres D.A., Goldstein J.L., Russell D.W., Brown M.S.;
RT	"cDNA cloning and expression of the peptide-binding beta subunit of
RT	p21ras farnesyltransferase, the counterpart of yeast DPrL/RAM1." ,
RL	Cell 66:321-334(1991) .
RN	[2]
RP	X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) .
RX	MEDLINE=97218306; PubMed=9065406;
RA	Park H.-W., Boduluri S.R., Moosaw J.F., Casey P.J., Beese L.S.;
RT	"Crystal structure of protein farnesyltransferase at 2.25-A
RT	resolution." ;
RL	Science 275:1800-1804(1997) .
RN	[3]
RP	X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS) .
RX	MEDLINE=98322062; PubMed=9657673;
RA	Long S.B., Casey P.J., Beese L.S.;
RT	"Co-crystal structure of protein farnesyltransferase complexed with a
RT	farnesyl diphosphate substrate." ;
RL	Biochemistry 37:9612-9618(1998) .
CC	-1- FUNCTION: CATALYZES THE TRANSFER OF A FARNESYL MOIETY FROM
CC	FARNESYL PYROPHOSPHATE TO A CYSTEINE AT THE FOURTH POSITION FROM
CC	THE C-TERMINUS OF SEVERAL PROTEINS. THE BETA SUBUNIT IS
CC	RESPONSIBLE FOR PEPTIDE-BINDING.
CC	-1- COFACTOR: BINDS ONE ZINC ION.

```
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
CC FAMILY
CC -1- SIMILARITY: CONTAINS 5 PFTB REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M69056; AAA41176.1; -.
DR PIR; A40037; A40037.
DR PDB; 1FT1; 18-MAR-98.
DR PDB; 1FT2; 18-NOV-98.
DR InterPro; IPR001330; Prenyltrans.
DR Pfam; PF00432; Prenyltrans; 5
KM Transferase: Prenyltransferase. Repeat; Zinc; 3D-structure.
FT REPEAT 123 164 PFTB 1.
FT REPEAT 174 215 PFTB 2.
FT REPEAT 222 263 PFTB 3.
FT REPEAT 270 312 PFTB 4.
FT REPEAT 332 374 PFTB 5.
FT METAL 297 297 ZINC.
FT METAL 299 299 ZINC.
FT METAL 362 362 ZINC.
SQ SEQUENCE 437 AA: 48673 MW: 41A9B6D79C0319A8 CRC64;

Query Match 39.1%; Score 942.5; DB 1; Length 437;
Best Local Similarity 43.1%; Pred. No. 8.3e-74;
Matches 197; Conservative 64; Mismatches 137; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAADPDLPR-----LTVQVDEOMKYEAVGDIYSLGGAAPNTKS 56
DB 12 PSSSPVSEPLYSLRPHARERLQDDSVETVSIIDAKVEIKIOVFSSY---KFNHLV 68
QY 57 IMELMRDHIETLTPGLRHMGRFVNDANRPWLCYWMVHPLALDEALDDELDDITD 116
DB 69 PRLVLOREHNFHRLRGKQLQDLADECDASRPLCYWILSHSELDELPQIVARDVQ 128
QY 117 FLARCDKDGYSGGPGOLPHLATTYAVNTLVYIGSERALSSINGNLVNFMLQKQDV 176
DB 129 FLRLCPSGPGGPGGPGVPHLAPYAAVNLCTIGREAVNYINREKLLQVLYSLKPD 188
QY 177 GARFMDGGEIDVRSATYASVNLIDFKLAKGVDYIARCOYIEGGIAGEPRAEYH 236
DB 189 GSFLLMVGGEVYRSATYASVNLITNPDLREGEAEIARCOYIEGGIAGEPRAEYH 248
QY 237 GGYTFEGGLAALLNLNPAEKVDLPGLGNVAFRQ-GVECGFGQRTNKLVDGYSFMOGA 295
DB 249 GGYTFEGGLAALLNLNPAEKVDLPGLGNVAFRQ-GVECGFGQRTNKLVDGYSFMOGA 306
QY 296 AFTOKITTVDTQLKSSYSCRRPGECDACSSSYGCAKSSSAVDYAFGPFQIQSNQ 355
DB 307 -----LPLRLHALLA-----OCDPALSMNH----- 328
QY 356 ICPHLFNIALQOYILLCSQVLEGLRDKPKNRDHYSCYLSGLAVSOVSAMTDTGSCP 415
DB 329 ---MFOALQLEIYILMKCCCPAGCLLDKPKSRDFHTCYCTGLSLIAOHFG---SGAM 381
QY 416 LPOHVLGPRSNLEPIHPLVNVNLKDYHTAEFSESE 452
DB 382 LHDVWKGVEYENLQPTHFVYVNLGPKVYIQAATTFLOK 418

RESULT 5
PFTB_HUMAN STANDARD: PRT; 437 AA.
ID PFTB_HUMAN AC P49356:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
```

```
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein farnesyltransferase beta subunit (EC 2.5.1.-) (CAAX
DE farnesyltransferase beta subunit) (NAS proteins prenyltransferase
DE beta) (Pase-beta).
GN FNTB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93264431; Pubmed=8494894;
RA Omer C.A., Kral A.M., Diel R.E., Prendergast G.C., Powers S.,
RA Allen C.M., Gibbs J.B., Kohl N.E.;
RT Characterization of recombinant human farnesyl-protein transferase:
RT cloning, expression, farnesyl diphosphate binding, and functional
RT homology with yeast prenyl-protein transferases.;
RL Biochemistry 32:5167-5176(1993).
RN [2]
RP SEQUENCE OF 51-437 FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=94102736; Pubmed=8276393;
RA Andres D.A., Mlatovich A., Ozcelik T., Wenzlau J.M., Brown M.S.,
RA Goldstein J.L., Francke U.;
RT cDNA cloning of the two subunits of human CAAX farnesyltransferase
RT and chromosomal mapping of FNTA and FNTB loci and related
RT sequences.;
RL Genomics 18:105-112(1993).
CC -1- FUNCTION: CATALYZES THE TRANSFER OF A FARNESYL MOIETY FROM
CC FARNESYL PYROPHOSPHATE TO A CYSTEINE AT THE FOURTH POSITION FROM
CC THE C-TERMINUS OF SEVERAL PROTEINS. THE BETA SUBUNIT IS
CC RESPONSIBLE FOR PEPTIDE-BINDING.
CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
CC FAMILY
CC -1- SIMILARITY: CONTAINS 5 PFTB REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L00635; AAA35854.1; -.
DR EMBL; L10414; AAA86286.1; -.
DR HSSP; 002293; 1FT2.
DR MIM; 134636; -.
DR InterPro; IPR001330; Prenyltrans.
DR Pfam; PF00432; Prenyltrans; 5
KM Transferase: Prenyltransferase. Repeat; Zinc.
FT REPEAT 123 164 PFTB 1.
FT REPEAT 174 215 PFTB 2.
FT REPEAT 222 263 PFTB 3.
FT REPEAT 270 312 PFTB 4.
FT REPEAT 332 374 PFTB 5.
FT METAL 297 297 ZINC (BY SIMILARITY).
FT METAL 299 299 ZINC (BY SIMILARITY).
FT METAL 362 362 ZINC (BY SIMILARITY).
FT METAL 283 283 ZINC (BY SIMILARITY).
SQ SEQUENCE 437 AA: 48773 MW: 8E8E571846146709 CRC64;

Query Match 39.0%; Score 940.5; DB 1; Length 437;
Best Local Similarity 43.1%; Pred. No. 1.2e-73;
Matches 197; Conservative 62; Mismatches 139; Indels 59; Gaps 7;

QY 5 POSTPTGDDPAADPDLPR-----LTVQVDEOMKYEAVGDIYSLGGAAPNTKS 56
DB 12 PSSSPVSEPLYSLRPHARERLQDDSVETVSIIDAKVEIKIOVFSSY---KFNHLV 68
```


DE Type II proteins geranylgeranyltransferase beta subunit (EC 2.5.1.-)
DE (Type II protein geranylgeranyltransferase beta subunit) (Ggtase-II-
DE beta) (PGGT) (YPT1/SEC4 proteins geranylgeranyltransferase beta
DE subunit).
GN BERT2.
OS Candida albicans (yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10231;
RA Ishii N., Aoki T., Aritaawa M.;
RT Molecular cloning of BERT gene from Candida albicans.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE TRANSFER OF A GERANYL-GERANYL MOIETY FROM
CC GERANYLGERANYL PYROPHOSPHATE TO PROTEINS HAVING THE C-TERMINAL
CC X-CC OR X-C-X-C, WHERE BOTH CYSTEINES MAY BECOME MODIFIED. ACTS
CC ON YPT1 AND SEC4 (BY SIMILARITY).
CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
CC FAMILY.
CC -1- SIMILARITY: CONTAINS 6 PPTB REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB021171; BAA35193.1; -
DR HSSP: Q02293; 1FT1.
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; prenyltrns: 5.
KM Transferase; Prenyltransferase; Repeat; Zinc.
FT REPEAT 15 55 PPTB 1.
FT REPEAT 62 104 PPTB 2.
FT REPEAT 122 163 PPTB 3.
FT REPEAT 170 211 PPTB 4.
FT REPEAT 223 264 PPTB 5.
FT REPEAT 271 313 PPTB 6.
FT METAL 249 249 ZINC (BY SIMILARITY).
FT METAL 251 251 ZINC (BY SIMILARITY).
FT METAL 301 301 ZINC (BY SIMILARITY).
SQ SEQUENCE 341 AA; 38460 MW; 24A89E11FF911488 CRC64;
Query Match 14.2%; Score 343.5; DB 1; Length 341;
Best Local Similarity 25.0%; Pred. No. 3.3e-22;
Matches 92; Conservative 65; Mismatches 138; Indels 73; Gaps 8;
QY 52 PATKSIEMELKRODHIEITPGLRHMPPARVYDANRPMLCYMWHPPLALLDEALDDOLE 111
DB 6 PEKVIILFD--KSRHVDYIYKQESHRSFEWLSSEHLRMNGVLGVYALLTME--LSALAO 62
QY 112 NDIIIDFLARC-QDRDGYSGGPGCLPHLATTVAAVNTLTGICSERALSSIN-----R 162
DB 63 QVIDIYIMLCMDKDTGAFCGSPKIDGHIISTLSALQVLKTYIOEQLVINDNESSNGKR 122
QY 163 GULYFMQMDVSGAFRMDGCEIDYRASYTAISVSLVNTIDFLAKVGCDYARCOT 222
DB 123 ERLIFETIGLQLPQSGFQGDYGEVDTRFYVYAVSSISLMLNLTDSIDTASAFIMQCFN 182
QY 223 YEGGJAGEPVAEHGYTFPGCLALLILNDEAEKVDPS---LIGVAFRQGVEC-GFQG 277
DB 183 FDCGGLPGSGESHAOYFCYGLALMKNLDDLVDENKVKVLLIDMLEROLVPSGGNG 242
QY 278 RTNKLVDCCYCFWOGAIAFTQKLITTVDKQLKSSYCKRPSGEDACSTSSYGCTAKSS 337
DB 243 RPEKLPDVCYSMWVLSISLIL-----KRK 266

QY 338 SAVDYAKGFDFIDQSNQIDGFLFNIALQDYITLLCQVLEGGIRDPKPKANDRHYSYCL 397
DB 267 MNVDLK-----ITLENFILTCDLNGGFSRPGNQTDVYHTCPAI 306
QY 398 SGLAVSQY 405
DB 307 ACLSLIDY 314
RESULT 8
PBT1_SCHPO STANDARD; PRT; 311 AA.
AC P46960;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type II protein geranylgeranyltransferase beta subunit (EC 2.5.1.-)
DE (Type II protein geranylgeranyltransferase beta subunit) (Ggtase-II-
DE beta).
GN PBT1 OR SPAC167.02.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96310627; PubMed=8740421;
RA Godfrey R., Davey J.;
RT "Sequence of pbt1, a gene for the beta subunit of the type-II
RT geranylgeranyltransferase from the fission yeast schizosaccharomycetes
RT pombe.";
RL Yeast 12:479-482(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Rieger M., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE TRANSFER OF A GERANYL-GERANYL MOIETY FROM
CC GERANYLGERANYL PYROPHOSPHATE TO PROTEINS HAVING THE C-TERMINAL
CC X-CC OR X-C-X-C, WHERE BOTH CYSTEINES MAY BECOME MODIFIED.
CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
CC FAMILY.
CC -1- SIMILARITY: CONTAINS 5 PPTB REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X92183; CAA63094.1; -
DR EMBL: AL035248; CAA22847.1; -
DR HSSP: Q02293; 1FT1.
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; prenyltrns: 5.
KM Transferase; Prenyltransferase; Repeat; Zinc.
FT REPEAT 54 95 PPTB 1.
FT REPEAT 102 143 PPTB 2.
FT REPEAT 150 191 PPTB 3.
FT REPEAT 197 239 PPTB 4.
FT REPEAT 246 288 PPTB 5.
FT METAL 224 224 ZINC (BY SIMILARITY).
FT METAL 226 226 ZINC (BY SIMILARITY).
FT METAL 276 276 ZINC (BY SIMILARITY).
SQ SEQUENCE 311 AA; 35092 MW; 2AB617FC769DB08 CRC64;
Query Match 13.6%; Score 327.5; DB 1; Length 311;

QY 275 FCGRTNKLVDGCTSPMOGAAIAFTOKLITIVDKOLKSSYCKRPSGCDACSTSSGCTAK 334
DB 225 LMGRRSKLPDVCYSWVWVSSLAIIIGRL----- 251
QY 335 KSSSAVDYAKFGFDETIQGSNOIGPLFNHIALQOYILICSGVLEGJLRDKPGKNRDHYSC 394
DB 252 ---DIMINER-----LTFEIIICODEKKGCGISIDRENEVDVFTTV 288
QY 395 YCLSGLAVSQYSAMTDGSCPLQHVAGPYSNLLEPIHPLY 435
DB 289 FGVAIGS-----LMGIDNLY-PIIDPLY 309

RESULT 10

PGTL_HUMAN STANDARD: PRT; 377 AA.

AC P53609;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Geranylgeranyl transferase type I beta subunit (EC 2.5.1.-) (Type I
protein geranyl-geranyltransferase beta subunit) (GGTase-I-beta).
GN PGCT1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta, and Kidney;
RX MEDLINE=94148804; PubMed=8106351;
RA Zhang F.L., Diehl R.E., Kohl N.E., Glibbs J.B., Giros B.,
RA Casey P.J., Omer C.A.;
RT cDNA cloning and expression of rat and human protein
geranylgeranyltransferase type-I.";
RL J. Biol. Chem. 269:3175-3180(1994).
CC -1- FUNCTION: CATALYZES THE TRANSFER OF A GERANYL-GERANYL MOIETY FROM
GERANYLGERANYL PYROPHOSPHATE TO PROTEINS HAVING THE C-TERMINAL
SEQUENCE CYS-ALIPHATIC-ALIPHATIC-X. ACTS ON THE RAC1, RAC2,
RAP1A AND RAP1B PROTEINS.
CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
FAMILY.
CC -1- SIMILARITY: CONTAINS 4 PPTB REPEATS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL: L25441; AAA35888.1; -
DR HSSP: Q02293; IPT1.
DR MIM: 602031; -
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; Prenyltrans. 5.
KW Transferase; Prenyltransferase; Repeat; Zinc.
FT REPEAT 144 186 PPTB 1.
FT REPEAT 193 234 PPTB 2.
FT REPEAT 245 284 PPTB 3.
FT REPEAT 291 333 PPTB 4.
FT METAL 269 269 ZINC (BY SIMILARITY).
FT METAL 271 271 ZINC (BY SIMILARITY).
FT METAL 321 321 ZINC (BY SIMILARITY).
SO SEQUENCE 377 AA; 42396 MW; 565CD9B6C087AADF CRC64;

Query Match 13.38; Score 320; DB 1; Length 377;
Best Local Similarity 26.58; Pred. No. 4e-20;
Matches 110; Conservative 62; Mismatches 121; Indels 122; Gaps 18;

QY 59 LELMRDHEIVLTGRLRMNGRAPHVLDANRPILCYWVHPALDLDEALDDLENDITDF 117
DB 18 LDFLNRHVRREFORCLQVLPERYSLETSLRLTAFALSGMLD-SLDVYKNDILEMI 76
QY 118 -----LARCQDKGYSG---GPGLP-----HLATTYAAVNTLVYTG 152
DB 77 YSLQVLPTEDRSNLRNRCGFRSSYLGIIPNPSKAPGTARPHYDSGHIMATYGLSCTVILG 136
QY 153 SPRALLSINRGNILNFM--LOMKVSGAF--RMDGSEIDVRSYTAISVSLVNT----LD 206
DB 137 DD--LSRVNKEACLAGLALQLED--GSFCAYEGSENDRRRYCASCICVHLNWSGMD 192
QY 207 FRLAGVDYIARCQYEGGIGAGEPYVAEAGGYTFCGLAALLILNEAEKV---DLPSLI 262
DB 193 MKKAI---TYIRKSYSDNGIAGAGLESHGSGTFCGIALCLCMKLEVFSEKLNRIK 249
QY 263 GWAFRQGVCEGFGGRTKKLVDCGCTSPMOGAAIAFTOKLITIVDKOLKSSYCKRPSGCD 322
DB 250 RKCIMRO--QNGYGRNRPKPDVTCSTWGA---TLKLTKI----- 285
QY 323 ACSTSSYCTAKKSSSAVDYAKFGFDETIQGSNOIGPLFNHIALQOYILICSGVLEGJLRD 382
DB 286 -----FOYTNF-----EKN-----RNYLSTODRLVCGFAK 311
QY 383 KPGKNRDHYHSCYCLSGLAVSQYSAMTDGSCPLQHVAGPYSNLLEPIHPLYNY 437
DB 312 WDSHPDALHAFVIGIGL-----SLMESSIC-----KVHPALNY 346

RESULT 11

PGTL_RAT STANDARD: PRT; 377 AA.

AC P53610;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Geranylgeranyl transferase type I beta subunit (EC 2.5.1.-) (Type I
protein geranyl-geranyltransferase beta subunit) (GGTase-I-beta).
GN PGCT1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94148804; PubMed=8106351;
RA Zhang F.L., Diehl R.E., Kohl N.E., Glibbs J.B., Giros B.,
RA Casey P.J., Omer C.A.;
RT cDNA cloning and expression of rat and human protein
geranylgeranyltransferase type-I.";
RL J. Biol. Chem. 269:3175-3180(1994).
CC -1- FUNCTION: CATALYZES THE TRANSFER OF A GERANYL-GERANYL MOIETY FROM
GERANYLGERANYL PYROPHOSPHATE TO PROTEINS HAVING THE C-TERMINAL
SEQUENCE CYS-ALIPHATIC-ALIPHATIC-X. ACTS ON THE RAC1, RAC2,
RAP1A AND RAP1B PROTEINS.
CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
FAMILY.
CC -1- SIMILARITY: CONTAINS 4 PPTB REPEATS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL: L24116; AAA17756.1; -
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; Prenyltrans. 5.

KM Transferase: Prenyltransferase; Repeat; Zinc.
FT REPEAT 144 186 PFTB 1.
FT REPEAT 193 234 PFTB 2.
FT REPEAT 245 284 PFTB 3.
FT REPEAT 291 333 PFTB 4.
FT METAL 269 269 ZINC (BY SIMILARITY).
FT METAL 271 271 ZINC (BY SIMILARITY).
FT METAL 321 321 ZINC (BY SIMILARITY).
SQ SEQUENCE 377 AA; 42414 MW; AADCC7301AA4011 CRC64;

Query Match 13.0%; Score 313; DB 1; Length 377;
Best Local Similarity 26.0%; Pred. No. 1,6e-19;
Matches 108; Conservative 64; Mismatches 121; Indels 122; Gaps 18;

OY 59 LELMRDHIEXLTPLGRHMGPAFHVLDANRPMVLCYMWVHPLALDLEALDDLENDIDF 117
D 18 LDFLRHVRFFRCLOVLPERYSLETSRLTAFALSGLDMLD-SLDVVKRDIIM 76
OY 118 -----LARCDDKGGYSG--GGQLP-----HATTYAVNLTVTIG 152
D 77 YSLQVLPTEDSNIDRCGFKRSSTLGIPEFNSKNPOTAPRYSGHIAMTYGLSCLIIIG 136
OY 153 SERAISTINRNLNFM--LQMKDVSGAF-RMHGGEIDVRASYTAISVASLVNI--LD 206
D 137 DD--LSRYDKACLAGLRALQLED--GSFCAYPEGSENMRFYCCASCICYMLNMMSGMD 192
OY 207 FLAKGVDDYIARQGTREGIAGEPYAEAHGGYTPCGLAAILLNEAEKV---DLPSLI 262
D 193 MKKAL---SYRRSMSTNDNLGAGAGLESHGGSTFCGISLCLMGKLEVEVSEKELNIX 249
OY 263 GWAFRGVGECEGFGKRTNKLVDGCSYFWOGAALAFQKLTITVDKOLKSSYCKRPSGED 322
D 250 RMCIMRQ--QNGYHGRPNKPYDTCYSFWGA---TLKLKLI----- 285
OY 323 ACSTSSYCTAKKSSAVDAKFGFDFEIQOSNIGPLFNHIALOOYIILCSQVLEGGRLD 382
D 266 -----FOYTNF-----EKN-----RNIILSTORLAVGGRAK 311
OY 368 KPGKRDIHYHCYCLGLAVSOYSAMTDSGCLPQHVAGPYSNLEPHLYNV 437
D 312 WDSHPDLAHYFGICGL---SLMESGIC-----KVHPALNV 346

RESULT 12
PFTB_CAEEL
ID PFTB_CAEEL STANDARD; PRT; 325 AA.
AC P41992;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable protein farnesyltransferase beta subunit (EC 2.5.1.-) (CAAX
DE farnesyltransferase beta subunit) (RAS proteins prenyltransferase
DE beta) (Frase-beta).
GN B0280.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Fulton L., Waterston R.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: CATALYZES THE TRANSFER OF A FARNESYL MOIETY FROM
CC FARNESYL PYROPHOSPHATE TO A CYSTEINE AT THE FOURTH POSITION FROM
CC THE C-TERMINUS OF SEVERAL PROTEINS. THE BETA SUBUNIT IS
CC RESPONSIBLE FOR PEPTIDE-BINDING (BY SIMILARITY).
CC COPACITOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -! SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY
CC SIMILARITY).
CC -! SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
CC FAMILY.
CC -! SIMILARITY: CONTAINS 5 PFTB REPEATS.

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U10438; AAA19080.1; -
DR WormRep: B0280.1; CE00735.
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; Prenyltrans; 5.
KW Hypothetical protein; Transferase; Prenyltransferase; Repeat; Zinc.
DR REPEAT 74 115 PFTB 1.
FT REPEAT 122 163 PFTB 2.
FT REPEAT 170 211 PFTB 3.
FT REPEAT 218 259 PFTB 4.
FT REPEAT 266 312 PFTB 5.
FT METAL 244 244 ZINC (BY SIMILARITY).
FT METAL 246 246 ZINC (BY SIMILARITY).
SQ SEQUENCE 325 AA; 36189 MW; AFAEF82E0FC729E8 CRC64;

Query Match 12.3%; Score 297.5; DB 1; Length 325;
Best Local Similarity 27.6%; Pred. No. 2.9e-18;
Matches 92; Conservative 55; Mismatches 145; Indels 41; Gaps 12;

OY 51 AAWNTSIMLEIMROHIEYLTPLGRHMGPAFHVLDAN--RPMVLCYMWVHPLALDLEALDD 108
D 20 SPN-----ELKDLHAFFINQYERKNR--SYHIAHEHLRVSGIVCVAMD-LSKOLER 71
OY 109 DLENDIIDFLARCDKPDKDGYSGGGQLPPLATYAAVNTLVITGS-ERA---LSSINRG 163
D 72 MSTEELIVNVIGCRNTDGGYGPARGHDSHLHTLCAVQTLIFNSIEKADADITSEYKVG 131
OY 164 NLXNFMLOMKVDSNFRMHGGEIDVRASYTAISVASLVNIIDFKLAKGVGIARQGT 223
D 132 -----LQEDP--GSFCGDSLGEVDYTRFTLCSLCHLGRSLTLNDSAVFELMKRYNT 183
OY 224 EGGIAGEPYAEAHGGYTPCGLAAILLNEAEKVDLPDLGWAFAFGVCEGFGSTNLY 283
D 184 DGGFTGPGSESHSGQIYCCVAGALAIAGRLDEIDRRTAEMLAFRCDDGGGNGHPRKLP 243
OY 284 DGCYSFMOGAALAFQKLTITV--VDKOLKSSYCKRPSGEDACSTSSYCTAKKSSAVDY 342
D 244 DVCYSMWVLASLAILGRNLFTSDAMKFTY-----ACQDDETGGFADRPDGCYSF 294
OY 343 AK--FGPDFIQOSNIGPLFNHIALOOYIILCS 373
D 295 LNNIQKFTFVLQSNV-----LATYKQLFECS 321

RESULT 13
CWG2_SCHPO
ID CWG2_SCHPO STANDARD; PRT; 355 AA.
AC P32434;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type I protein geranyl-geranyltransferase beta subunit (EC 2.5.1.-)
DE (Type I protein geranyl-geranyltransferase beta subunit) (GGTase-I-
DE beta) (PGGT).
GN CWG2 OR SPAC21P5.04C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94083400; PubMed=8262067;
RX Diaz M., Sanchez Y., Bennett T., Dun C.R., Godoy C., Tamanoi F.,
RA Duran A., Perez P.;

RT The Schizosaccharomyces pombe cwg2+ gene codes for the beta subunit
RT of a geranylgeranyltransferase type I required for beta-glucan
RT synthesis.
RL EMBL J. 12:5245-5254(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-972.
RA Harris D., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE TRANSFER OF A GERANYL-GERANYL MOIETY FROM
CC GERANYLGERANYL PYROPHOSPHATE TO PROTEINS HAVING THE C-TERMINAL C-
CC A-A-L. IN PARTICULAR IT MODIFIES THE GTP-BINDING COMPONENT OF THE
CC (1-3)-BETA-D-GLUCAN SYNTHASE.
CC -1- COPROCTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
CC FAMILY.
CC -1- SIMILARITY: CONTAINS 3 PFTB REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z12155; CAA78143.1; -.
DR EMBL: AL163071; CAB86347.1; -.
DR PIR: S41686; S41686.
DR HSSP: 002293; 1PT1.
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; Prenyltrans; 4.
KW Transferase; Prenyltransferase; Repeat; Zinc.
FT REPEAT 169 210 PFTB 1.
FT REPEAT 234 275 PFTB 2.
FT REPEAT 282 324 PFTB 3.
FT METL 260 260 ZINC (BY SIMILARITY).
FT METL 262 262 ZINC (BY SIMILARITY).
FT METL 312 312 ZINC (BY SIMILARITY).
SQ SEQUENCE 355 AA; 40023 MW; 811A3CBF067071 CRC64;

Query Match 12.0%; Score 289.5; DA 1; Length 355;
Best Local Similarity 28.1%; Pred. No. 1.6e-17;
Matches 116; Conservative 47; Mismatches 137; Indels 113; Gaps 16;

OY 59 LELMNDQHIETVLTGRLKMGAFHVLNANRPLCYMWHPLLD--EALDDLENDIID 116
DB 1 MELTRAKHIAFKRHLLEPPRYEHCERTVLAFCCLGLDLNLNTIDDKRSMIE 60
OY 117 FLAR-----CODKDGSGSGSP-----QLPHLATTAAVNTLTIGSEDLSSIN 161
DB 61 WIKKNVTKESGKIKYSGFQAYRTGIQIPISBEPQIAGVPSICGLRLGN--LSRID 118
OY 162 RGNLTNFMLOMKDVGAR---MHDGEIDVRASYTRIASVSLVNLIDKRLAKGCG--DY 216
DB 119 RLLNFEVLCTSGGHRHRSIAVSCSDQDMRLQYMAVTTASL--LDFSLSDPLCSIOY 175
OY 217 IARQTYEGGIAGEPYAEPYAEAGTYFCGLA--ALIL-----LNEAE-----KVD 257
DB 176 IKSCORVEGGSFLPYGEAHAGATFCALASMSLILKMPSSLNTSNGSYNLMDCPVPE 235
OY 258 LPSLIGWAFAGQVEGCGGRTNKLYGCGSFMQNAALAFQTLITIVDKOLKSSYCKR 317
DB 236 --RLRKLWLASQLSSGGINGTNTNADVTCYAV--VLSSKLL-----274
OY 318 PSGEDACSTSSVCGTANKSSAVDYAKGFDFIQSNOIQPLFHNTALQOYIILCSQYLE 377
DB 275 ----DAL-----PFDIGGELEKYLILHAQNAL 297
OY 378 GGLRDKPGKNRQHYHSCYCLSLAVSIOYSAMTDGSCPLPO---HYLGYSNL 427
DB 298 GGFSTPDEFPDVLHSLGLTAMAYO-----DCKSPKVVNADIRHTSKYINI 344

RESULT 14
PCTB_RAT ID PCTB_RAT STANDARD; PRT; 331 AA.
AC 008603;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Geranylgeranyl transferase type II beta subunit (EC 2.5.1.-) (RAB
DE geranylgeranyltransferase beta subunit) (RAB geranyl) (RAB
DE geranyltransferase beta subunit) (RAB GG transferase beta) (RAB GGase
DE beta).
GN RABGGB OR GGTB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93280201; PubMed=8505342;
RA Armstrong S.A., Seabra M.C., Suedhof T.C., Goldstein J.L.,
RA Brown M.S.;
RT cDNA cloning and expression of the alpha and beta subunits of rat
RT Rab geranylgeranyl transferase.
RT J. Biol. Chem. 268:12221-12229(1993).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=95083621; PubMed=7991565;
RA Farnsworth C.C., Seabra M.C., Ericsson L.H., Gelb M.H., Glomset J.A.;
RT Rab geranylgeranyl transferase catalyzes the geranylgeranylation of
RT adjacent cysteines in the small GTPases Rab1A, Rab3A, and Rab5A.
RL Proc. Natl. Acad. Sci. U.S.A. 91:11963-11967(1994).
CC -1- FUNCTION: CATALYZES THE TRANSFER OF A GERANYL-GERANYL MOIETY FROM
CC GERANYLGERANYL PYROPHOSPHATE TO BOTH CYSTEINES IN RAB PROTEINS
CC WITH AN -XKCC, -XKCC AND -CCXX C-TERMINAL, SUCH AS RAB1A, RAB3A
CC AND RAB5A RESPECTIVELY.
CC -1- COPROCTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- ENZYME REGULATION: THE ENZYMATIC REACTION REQUIRES THE AID OF A
CC RAB ESCORT PROTEIN (ALSO CALLED COMPONENT A).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT, COLLECTIVELY
CC CALLED COMPONENT B.
CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN THE HEART, BRAIN, SPLEEN AND
CC LIVER. LESS IN THE LUNG, MUSCLE, KIDNEY AND TESTIS; IN THESE
CC TISSUES, MORE ABUNDANT THAN THE ALPHA SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
CC FAMILY.
CC -1- SIMILARITY: CONTAINS 6 PFTB REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L10416; AAA41999.1; -.
DR EMBL: S62097; AAB27019.1; -.
DR PIR: B45977; B45977.
DR HSSP: 002293; 1PT1.
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; Prenyltrans; 5.
KW Transferase; Prenyltransferase; Repeat; Zinc.
FT REPEAT 20 61 PFTB 1.
FT REPEAT 68 109 PFTB 2.
FT REPEAT 116 157 PFTB 3.
FT REPEAT 164 205 PFTB 4.
FT REPEAT 212 253 PFTB 5.
FT REPEAT 260 302 PFTB 6.
FT METL 238 238 ZINC (BY SIMILARITY).
FT METL 240 240 ZINC (BY SIMILARITY).

Mon Nov 4 12:24:41 2002

us-09-786-675-12.rsp

Page 12

```
OY      410 DTGSCPLPQHVLGPRYSNLEPIRHELY---NVVLDKYHTAVEEFS 450
          ::|| ::||::|::|::|::|::|::|::|::|::|::|::|::|
Db      300 -----LLG--EQQIKPVRNVFPCMRPEVYLQVRVNVQPELVS 331
```

Search completed: November 1, 2002, 18:07:53
Job time : 23 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2002, 17:09:05 ; Search time 62 Seconds
(without alignments)

1261.189 Million cell updates/sec

Title: US-09-786-675-12

Perfect score: 2411
Sequence: 1 MDPSPSTPTPTGDDPAAD.....PLYNVLDKHTAFEPSEE 452

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPRMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1357.5	56.3	470	10 P93228	P93228 Lycopersico
2	1353.5	56.1	470	10 P04679	004679 Lycopersico
3	1345	55.8	446	10 O24448	024448 nicotiana 9
4	832.5	34.5	419	5 O9VEV7	09vev7 drosophila
5	805.5	33.4	401	5 O19752	019752 caenorhabdi
6	623.5	25.9	382	3 O13782	013782 schizosacch
7	531.5	22.0	585	5 O9NC76	09nc76 trypanosoma
8	342.5	14.2	375	10 O9FMP2	09fmp2 arabidopsis
9	342.5	14.2	375	10 O80642	080642 arabidopsis
10	336	13.9	317	10 O9LHLS	09lhls arabidopsis
11	322.5	13.4	376	10 O9FPP6	09fpp6 arabidopsis
12	304.5	12.6	347	5 O9X268	09x268 drosophila
13	287	11.9	395	5 O24172	024172 drosophila
14	286	11.9	395	5 O24173	024173 drosophila
15	244.5	10.1	360	5 O18197	018197 caenorhabdi
16	218	9.0	237	11 O9CRG6	09crg6 mus musculu

17	184	7.6	398	3 O9Y764	O9y764 candida alb
18	168.5	7.0	358	10 O9IGK1	O9igk1 oryza sativ
19	116	4.8	80	5 O9NIV6	O9niv6 leishmania
20	106.5	4.4	514	10 O9FRM9	O9frm9 nepenthes a
21	102.5	4.3	410	10 O9LFD4	O9lfd4 arabidopsis
22	102.5	4.3	553	10 O9FVY9	O9fvy9 oryza sativ
23	100	4.1	494	10 O9FVSO	O9fvs0 arabidopsis
24	97	4.0	503	5 O25412	O25412 lymnaea sta
25	96.5	4.0	502	10 O94130	O94130 oryza sativ
26	96	4.0	1716	13 O91932	O91932 cyrtinus ca
27	94	3.9	2183	12 O91ON8	O91on8 meases vir
28	93.5	3.9	2155	4 O75443	O75443 homo sapien
29	93.5	3.9	2512	16 O10896	O10896 mycobacteri
30	92.5	3.8	231	11 O921H9	O921h9 mus musculu
31	92.5	3.8	262	5 O9V9S0	O9v9s0 mycobacteri
32	92.5	3.8	346	16 O05805	O05805 mycobacteri
33	92.5	3.8	585	10 O9FPW1	O9fpw1 symbiodiniu
34	92	3.8	365	4 O96DL1	O96dl1 homo sapien
35	92	3.8	374	2 O938Y4	O938v4 bradyrhizob
36	92	3.8	1348	5 O9YAD1	O9yad1 drosophila
37	92	3.8	1392	5 O957D7	O957d7 drosophila
38	92	3.8	1998	5 O9V7A5	O9v7a5 drosophila
39	91.5	3.8	791	4 O9UF44	O9ufa4 homo sapien
40	91	3.8	347	16 O225S1	O225s1 rhizobium m
41	91	3.8	499	2 O9AUE4	O9aue4 klatscospo
42	90.5	3.8	271	17 O28729	O28729 archaeoglob
43	90.5	3.8	325	17 O9HKA0	O9hka0 thermoplasm
44	90.5	3.8	802	4 O96PU4	O96pu4 homo sapien
45	90	3.7	608	2 O9ZBW6	O9zbw6 streptomyce

ALIGNMENTS

RESULT 1

P93228 ID P93228 PRELIMINARY; PRT; 470 AA.
AC P93228;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FARNSYLV PROTEIN TRANSFERASE SUBUNIT B.
GN LEFTB.
OS Lycopersicon esculentum (tomato)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV_VENT CHERRY LA1221.
RX MEDLINE=972199868; PubMed=9121446.
RA Yalovsky S., Trueblood C.E., Callan K.L., Jenkins S.M.,
RA Rine J., Gruissem W.;
RT "Plant farnesyltransferase can restore yeast Ras signaling and
RT mating";
RL Mol. Cell. Biol. 17:1986-1994(1997).
DR EMBL: U83708; AAC49666.1; -
DR HSSP: 002293; 1FT1.
DR InterPro: IPR001330; Prenyltrans.
DR InterPro: IPR00169; Thiolprot_act_site.
DR Pfam: PF00432; Prenyltrans; 5.
DR PROSITE: PS00639; THIOL_PROTEINASE_HIS; UNKNOWN_1.
KW TRANSFERASE.
SQ SEQUENCE 470 AA; 52220 MW; E5FEDD582B074D3B CRC64;

Query Match 56.3%; Score 1357.5; DB 10; Length 470;
Best Local Similarity 57.3%; Pred. No. 1.2e-115;
Matches 226; Conservative 68; Mismatches 100; Indels 23; Gaps 3;

QY 25 RLTVQVEQMKVAVNGDIYSLFGAENKSLMLEWRDQHEVLTPLGRHNGPAFHVLT 84
DB 5 KYVKLEDDQVVERVREIYDFYVSNPSDILFIEDKHKRGYLSGCRKLKSGSVLT 64

[illegible]

RESULT 2	PRELIMINARY:	PRT:	470 AA.
004679			
ID	004679		
AC	004679;		
DT	01-JUL-1997 (TREMBLrefl. 04, Created)		
DT	01-JUL-1997 (TREMBLrefl. 04, Last sequence update)		
DT	01-DEC-2001 (TREMBLrefl. 19, Last annotation update)		
DE	PARMESYL-PROTEIN TRANSFERASE BETA SUBUNIT.		
GN	LEPTB.		
OS	Lycopersicon esculentum (Tomato).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Asteridae; euasterids I; Solanales; Solanaceae; Solanum.		
OX	NOBL_TaxID=4081;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TRANSDOSON=LEFTB-SOL3;		
RX	MEDLINE=97422406; PubMed=9278174;		
RA	Rebalchouk D., Narita J.O.;		
RT	"Foldback transposable elements in plants.";		
RL	Plant Mol. Biol. 34:831-835(1997).		
DR	EMBL: U75644; AAB69757.1; -.		
DR	HSSP: Q02293; IPr1.		
DR	InterPro: IPR001330; Prenyltrans.		
DR	InterPro: IPR000169; Thiolprot_act_site.		
DR	Pfam: PF004432; prenyltrans_5		
DR	PROSITE: PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.		
DR	Transferase.		
QO	SEQUENCE 470 AA: 52215 MW: 74976F8344911345 CRC64;		

Query Match	56.1%;	Score 1353.5;	DB 10;	Length 470;
Best Local Similarity	57.3%;	Pred. No. 2.9e-115;		
Matches 256;	Conservative 67;	Mismatches 101;	Indels 23;	Gaps 3

[illegible]

Db	125	VNSLITLGRPEALSSINRERKLYTFLRLRKDASGGFRMHGGEVDYRACVYTIASVANTILNI	184
Oy	205	LDPRLKAGVDYIARORRYEGGJINGEPAAEHGCGYPCGIAALITLNEAEKVDPLSLTGM	264
Db	185	VYDELLHGVGNITLSCQYIEGGIAGEPSEAHGGITPFCGLAMILLINEYNRNLDELGLDM	244
Oy	265	VAFRGVGGCFQGRITKLIVDGCYSFHWQCAALIAFTQKLITTVDKLSSYSYCKRPSGEDAC	324
Db	245	VYFRQGVGGFQGRITKLIVDGCYSFHWQCAVAVFLIQRINLIYHSQLSLSDLSSTESADSS	304
Oy	325	ST-----SSY-----GCTAKKSSSAVDYAKFGFDFIQSSNOIQPLFHN	362
Db	305	ESELSDDEEHLEGISHSQDTFPLQAGACQENASHSPIADTQGYEFIRPLAKRPLFDS	364
Oy	363	IATQYITLCSQVLEGGADRKGKKNRPHYSYCSLGSIAVSOYSAMTDRGSCPLPQNYLG	422
Db	365	MYLDQYVILCSQIENVGGRDRKGRGROYIYHCTCLSLSTIAQYSMTDENSDSPPLPRDVG	424
Oy	423	PYSN-LLEPLHPLNYVYLDKXHTAVER	448
Db	425	PYSKCLLEQVHPLFNVLVDYRYEAERY	451

```

RESULT 3
ID 024448 PRELIMINARY; PRT: 446 AA.
AC 024448;
DT 01-JAN-1998 (TRENBLREL, 05, Created)
DT 01-JAN-2000 (TRENBLREL, 05, Last sequence update)
DT 01-DEC-2001 (TRENBLREL, 19, Last annotation update)
DE FARNESYLTRANSFERASE BETA SUBUNIT (EC 2.5.1.21) (FRAGMENT).
OS NICOTIANA GLUTINOSA (Tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=35889;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou D., Yang Z., Cramer C.L.;
RT "A cDNA Clone Encoding the beta Subunit of Protein Farnesyltransferase
   from Nicotiana glutinosa (Accession No. U73203) (FGR96-109).";
RL Plant Physiol. 112:1396-1398(1996).
DR EMBL: U73203; AAB8796.1; -.
DR HSSP: Q02293; 1PFI.
DR InterPro: IPR001330; PrenylTrans.
DR InterPro: IPR000169; ThiolProt_act_site.
DR Pfam: PF00432; PrenylTrans_5.
DR PROSITE: PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
KM Transferase.
QT NON_TER 1
SQ SEQUENCE 446 AA: 49749 MW: 975694926437A05 CRC64;

```

Query Match	55.8%	Score 1345;	DB 10;	Length 446;
Best Local Similarity	58.6%;	Pred. No. 1.6e-114;		
Matches 260; Conservative	60;	Mismatches 100;	Indels 24;	Gaps 6;

[illegible]

```

OY 267 FRQGVGCGFQGRNTKLVDCGYSFMOGAIAFTQKLTITVDKQKSSYSCRRPSGDC-- 324
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 242 FRQGVGSGFGQGRNTKLVDCGYSFMOGAIAFTQKLTITVDKQKSSYSCRRPSGDC-- 301
OY 325 -----STSSY---GCT-----AKSSAVDYAKFGFDFIOGNOICPLPHNIALQO 367
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 302 ELSDHEHLQGGTSHVQKTCPLGCGQENASDPKRIADTCYDFNRIARPFDSFYIQO 361
OY 368 YLLCSQVLEGLRDKPGKNDHYHSCYCSGLAVSOYSAMTDTGSCPLPOHVLGPYS-N 426
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 362 YLLCSQI--DGFGRDKPGKNDHYHSCYCSGLAVSOYSAMTDTGSCPLPOHVLGPYS-N 420
OY 421 LLEPHLPYLVLDKRYHTAFEFES 450
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 421 LLEPHLPYLVLDKRYHTAFEFES 444

RESULT 4
OYEV7 PRELIMINARY; PRT; 419 AA.
AC OYEV7
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CG17565 PROTEIN (L036454P).
GN CG17565.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyridioidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Goeys J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrelira S., Fleischmann W.,
RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitai M., Kalush F., Kapran G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasno P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paolel J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RL "The genome sequence of Drosophila melanogaster."
RT The genome sequence of Drosophila melanogaster.

```

```

RN [2]
RC STRAIN-Y, CN BW SP;
RA Stapleton M., Brockstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez J., Guarini H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Paolel J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celiker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003713; AAF55310.1;
DR EMBL; AY051869; AAK93293.1;
DR HSSP; Q02293; IFT2.
DR Flybase; FBgn0038424; CG17565.
DR InterPro; IPR001330; Ptenyltrans.
DR Pfam; PF00432; Ptenyltrans; 5.
SQ SEQUENCE 419 AA; 46711 MW; 431E0E5275167B98 CRC64;

Query Match
Best Local Similarity 34.5%; Score 832.5; DR 5; Length 419;
Matches 180; Conservative 54; Mismatches 134; Indels 63; Gaps 6;

OY 27 TYTOYEQMKVEARVG---DIYRSIFGAAPNTKSIIMEIWRDHIEXLTPGLRMGPAPHV 83
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 27 TTSRROQKTESSEYKCEPDFEQIMFTDPR---LTQIFRLHQYVLDMRLPSNVEC 82
OY 84 LDANRPWLCYMWVHPLALDLDELDLNDIIDLFLARCQDKGSGGSGOLPLATTYA 143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 83 LQSSRAMCYMTWILQAAQLSNFDDQTLNHVQFLSNCKRSPTEFGFGEGYAHALPYTA 142
OY 144 AVNTLVTTIGSERALSSINRGNLYNFMLOMKDVSCAFRMDHGBEIDVRASYTA1SVASLVN 203
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 143 AVNSLCIIGSEQQYRAIDRPLTVQFLFSVRSDSPFLHVDGETDVRGAYCAISCAKLLN 202
OY 204 ILD---FKLAKGVGYIARCOYREGTAGEPYAHAGGYFGCGALJILNEAKVDLPS 260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 203 LEPYVKEIFPATQGWIMACQTYEGGREGARGLAHHGTYFCGICAGLALLNENKCDQRA 262
OY 261 LIGWAFFRO-GVECSFGQGRNTKLVDCGYSFMOGAIAFTQKLTITVDKQKSSYSCRRPS 319
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 263 LKWLRLRQMTYEGCGFQGRNTKLVDCGYSFMOGAIAFTQKLTITVDKQKSSYSCRRPS 315
OY 320 GEDACSTSSGCTAKSSAVDYAKFGFDFIOGNOICPLPHNIALQOYIILCSQVLEGG 379
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 316 -----LFEVALQETIILCCQKQSG 336
OY 380 LRDKPGKNDHYHSCYCSGLAVSOYSAMTDTGSCPLPOHVLGPYSNLLPHLPYLVN 439
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 337 LIDKPGKNDHYHSCYCSGLAVSOYSAMTDTGSCPLPOHVLGPYSNLLPHLPYLVN 390
OY 440 DKYHTAFEFES 450
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 391 KSYAARSHFS 401

RESULT 5
AC 019752 PRELIMINARY; PRT; 401 AA.
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE F23812.6 PROTEIN.
GN F23812.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN 11
RP SEQUENCE FROM N.A.
RA Wild A.,
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RT The genome sequence of Drosophila melanogaster.

```

RA MEDLINE=99069613; PubMed=9851916;
RX none;
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology";
RT Science 287:2012-2018(1998).
RL EMBL: Z77659; CAB0167.1; -;
DR HSSP: Q02293; IPT1.
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; Prenyltrans; 6.
SQ SEQUENCE 401 AA; 45093 MW; D767D7C3698BD1A CRC64;

Query Match 33.48; Score 805.5; DB 5; Length 401;
Best Local Similarity 38.98; Pred. No. 3.4e-65;
Matches 169; Conservative 73; Mismatches 135; Indels 57; Gaps 6;

QY 22 LPLRLTVGEQMKVEARVDYRSL----FGAAPNTKSTMLEMRDQHEYLTPGLRHIM 77
DB 18 DDNPFYSTEDCKRIETMIFENYNSYLEPDKTTSDEDLAELTIFPQKHASYLLRYLKNC 77
QY 78 GPAFVLDANRPMLCYMWVHPALDLDEALDDLENDIIDFLARCQDKDGSGGPGQLPH 137
DB 78 PSSVATLDASRSMCKGVNMLKILDAEIPRDYENTIVYFKCEHPREGCGGQQLAH 137
QY 138 LATTVAANTLVITIGSERALSSINRGLYNFMLOKMDVSCAFRMDGGEIDVRASTYALS 197
DB 138 LAPTYAAVMCLVSLQKEBALRSINRVTLFNFKCKHESGSGFYMHGGEIDMRSAVCALA 197
QY 198 VASVILIDFLKAGVGYIARCQYEGTAGEPYARAHGTYFGCLALILINAEKVD 257
DB 198 TCEIYVGLPDELSNGVAEMITSCSPFEGGEGEPTTAHGTYFCVAVSLVILNRFRLAD 257
QY 258 LPSLIGMAVFRQ-GVECGFGQRTKLVDCGSEWQGAIAFTQKLTIVDKQLSSYSCK 316
DB 258 MGLLWMATRRQMRREGFGQRTKLVDCGSEWQGA-----IFPLDGEHEBE--- 306
QY 317 RPSGEDACSTSSGCTAKKSSSAVDYAKFGDFIQGNOIGPLEFHIALQOYLILCSOYL 376
DB 307 -----GRSLKSG-----LFEARMLKEVITLVCCOSY 331
QY 377 EGGLEDKPKKNNDHYHSCYGLSLGAVSOYSAMDTGSCPLPOHVLGPNYSLLEPIPLYNV 436
DB 332 HGGFEDKPKDPVLDYHTYVLSGLSVAKYSLARDK-----TLGGDVNMLAETINPVFN 385
QY 437 VVLDKYHFFAYEFS 450
DB 386 VVTASGFQAKKEFT 399

RESULT 6
ID 013782 PRELIMINARY; PRT; 382 AA.
AC 013782;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (EC 2.5.1.-)
DE (CAAX FARNESYLTRANSFERASE BETA SUBUNIT)
DE (RAS PROTEIN PRENYLTRANSFERASE) (FPAE-BETA).
GN SPAC1766.04C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Murphy L., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE BETA SUBUNIT IS RESPONSIBLE FOR PEPTIDE-BINDING.
CC -1- CORACOR: CONTAINS A CATALYTIC ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY
SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE PROTEIN PRENYLTRANSFERASE BETA SUBUNIT
CC FAMILY.
DR EMBL: Z99162; CAB16215.1; -;
DR HSSP: Q02293; IPT2.
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; Prenyltrans; 5.
KW Hypothetical protein; Transferase; Prenyltransferase; Repeat; Zinc.
FT METAL 253 253 ZINC (BY SIMILARITY).
FT METAL 255 255 ZINC (BY SIMILARITY).
FT METAL 316 316 ZINC (BY SIMILARITY).
SQ SEQUENCE 382 AA; 42188 MW; C3F2705D33F84203 CRC64;

Query Match 25.98; Score 623.5; DB 3; Length 392;
Best Local Similarity 36.26; Pred. No. 1.5e-48;
Matches 152; Conservative 61; Mismatches 144; Indels 63; Gaps 10;

QY 23 LPLRLTVGEQMKVEARVDYRSLFGAAPTNTKSTMLEMRDQHEYLTPGLRHIMGPAFH 82
DB 1 MDLSETOYQNETATVPLPLNG-----ESQSPNLQ-----KHLKYLTKMLDPLPSFT 50
QY 83 VLDANRPMLCYMWVHPALDLDEALDDLENDIIDFLARCQDKDGSGGPGQLPHLATTY 142
DB 51 VLDASRMMVWVWELSSIALILK-LDSSVCERALSIVNOLKPGSGCGGQNDLHLLSTY 109
QY 143 AAVNTLVITIGSERALSSINRGLYNFMLOKMDVSCAFRMDGGEIDVRASTYALS 202
DB 110 ASILSLICLDSTDAVSLERDLVDFSLKNDGSRVNNEDSADARSVAAYCVSSLY 169
QY 203 NI-LDFKLAKGVGYIARCQYEGTAGEPYARAHGTYFGCLALILINAEKVDLPSL 261
DB 170 GISMDPLFEGLTQWLCQYEGTAGEPYARAHGTYFCVAVSLVILNRFRLAD 229
QY 262 IGVAFRQGVCEC-GFGQRTKLVDCGSEWQGAIAFTQKLTIVDKQLSSYSCKRSPG 320
DB 230 STMIVQRODPALYGFSGRSKLVDCGSEWQGAIAFTQKLTIVDKQLSSYSCKRSPG 267
QY 321 EDACSTSSGCTAKKSSSAVDYAKFGDFIQGNOIGPLEFHIALQOYLILCSOYL 379
DB 268 -----ASGYSASHS-----LPNLFYNEKLLGYILQCCSTSGG 303
QY 380 LRDKPKKNNDHYHSCYGLSLGAVSOYSAMDTGSCPLPOHVLGPNYSLLEPIPLYNV 437
DB 304 LRDKPKPKRDYHTYVLSGLSVAKYSLARDK-----TLGGDVNMLAETINPVFN 362

RESULT 7
ID 09NC76 PRELIMINARY; PRT; 585 AA.
AC 09NC76;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT.
OS Trypanosoma brucei brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ISTAR 1.7;
RA Buchner F.S., Yokoyama K., Nguyen L.N., Grewal A.,
RA Erdjument-Bromage H., Tempst P., Strickland C.L., Xiao L.,
RA Van Voorhis W.C., Gelb M.H.;
RT "Cloning, heterologous expression, and distinct substrate specificity
of protein farnesyltransferase from Trypanosoma brucei";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF230369; AAF3920.1; -;
DR HSSP: Q02293; IPT1.
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; Prenyltrans; 5.
KW Transferase.
SQ SEQUENCE 585 AA; 65432 MW; 75689958DE68B09 CRC64;

Query Match 22.08; Score 531.5; DB 5; Length 585;

Best Local Similarity 29.2%; Pred. No. 7.5e-40;
Matches 148; Conservative 67; Mismatches 169; Indels 123; Gaps 14;

QY 53 NTKSMLEMDHOIEYLTQLRHMGAFVLDANRPWLCYMWVHPLALL-----102
Db 61 NEEGVHSLNRESHEKLSRLVYKLEPYAORLYNAPMVMYVTLAAEALGITEKLYDOI 120
QY 103 -----DEALDDLE-----NDIIPILACODKDG--126
Db 121 SODALGERILSLDQPEYDEQKCGKMGSEBGGKMGKSPQOCCGVNYPDLARC-DADHTC 179
QY 127 --GYSGGC-GGLPLATTYAANVTLTIGSERLSSINGNLNFMLOKDYSCAFRMD 183
Db 180 AIGFSGGWGQIPHLATSYAGVCSLILGCPREYLOALPSPAIRKRWLLSLRCADGSPFRMI 239
QY 184 GGEIDVRASTVAISVSLVNLDFKLAKG-----VGDYIARCOYEGGIA-GEPIYARAH 236
Db 240 GGEADIRASVCVAVITTLQLOVDVRSGLILREDAQAVASQTHHEGSGFACGRASDAH 299
QY 237 GGYTCGIALIILNEAEKVDLSLIGVAFRQ-GVECGPQGRTKLVDCYSFMOGA- 294
Db 300 GATYOCGLAALILKRPCLCNTRALRGMLAAROLRPEGNGNTNKLVDSCYAHWVASH 359
QY 295 -----IAFTOKLITTYDKOLKSSYCKRPSGEDACS-----T 326
Db 360 VLLRYGESLAKITTCGETKRSLSREMLLDHAQLVDISNLHPESFAMSHHEEKQERA 419
QY 327 SSYCGTAKSSSAVDYAKPFDPFIQOSNOIGPLFNHIALQOYILLCQVL-EGCLRDPC 385
Db 420 SRVEAYLSATPLAASWSSSGVPVNLDDAGDFTFNORLQLYLILCCQORREGGLMDPN 479
QY 386 KNRDHYSCYGLAVSQ-----YSAMTDIGSCP-----LP 417
Db 480 YPNDFYHCTSLSCMSASQNOGQVNRDGRDLSCGNSFYAALSRGTYIGRDSYGIYP 539
QY 418 OHVLGPTVS-----NLLEPIHPLXNY 437
Db 540 SDEKSGVSSELHLSKNCILRPNPLFNI 566

RESULT 8
Q9FMP2 PRELIMINARY; PRT; 313 AA.
AC Q9FMP2:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE RAB GERANYLGERANYLTRANSEFERASE, BETA SUBUNIT.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
RN NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE-98162728; PubMed-9501997;
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT Sequence features of the regions of 1,191,918 bp covered by seventeen
RT physically assigned pl clones.";
RL DNA Res. 4:401-414(1997).
DR EMBL: AB007727; BABI0039.1; -;
DR HSSP: 002293; IPTI.
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; prenyltrans; 5.
DR Transferase.
SQ SEQUENCE 313 AA; 34700 MW; 4258895012A6B29 CRC64;

Query Match 14.2%; Score 343.5; DB 10; Length 313;
Best Local Similarity 27.18; Pred. No. 4.8e-23;
Matches 95; Conservative 60; Mismatches 131; Indels 65; Gaps 8;

QY 58 MLEIMRDHOIEYLTQGLRHMGAFVLDANRPWLCYMWVHPLALLDEALDDLENDIT 115
Db 1 MVLVAADHVRITLMAEKKK-ESFESVYKMDLHRNGAWGLTTLDDLK-LGCVSEEEVT 58
QY 116 DFLARCDKDGSGSGGQPLPHLATTYAANVTLTIGSERLSSINGNLNFMLOKDYSCAFRMD 175
Db 59 SWLMTCOHESGGFGFNGNCHDPHILYTLTSAVQIALFLPK--INILDIGVSSYAKLQNE 115
QY 176 SGAFRMDHGGEDVRASTVAISVSLVNLDFKLAKGVDYIARCOYEGGIAEPIYAE 234
Db 116 DGSFSGDMNGEIDRPFSTALICLSIIKCLDKINVEKAV-KYIVSCNKLDSGFQCTPGAE 174
QY 235 AHGQYFCGLAALILNEAEKVDLSLIGVAFRQGEVCGPQGRTKLVDCYSFMOGA 294
Db 175 SHAGQIFCCVGAIALITGSLHHVDKDSGLMWLCEKQLKAGLNGRPEKLADVCSYMWVLS 234
QY 295 IAFYOKLITTYDKOLKSSYCKRPSGEDACSTSSYCGTAKSSANDYAKPFDPFIQOSN 354
Db 235 LMDIV-----HWIDRAK-----248

QY 355 QIGPLFNHIALQOYILLCQVLEGLRDKPKNRDHYSCYGLAVSQY 405
Db 249 -----LVKFTLDCODLDNGISDRPDAVIDFHTFYGVAGLSLLEY 289

RESULT 9
O80642 PRELIMINARY; PRT; 375 AA.
AC O80642:
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PUTATIVE GERANYLGERANYL TRANSFERASE TYPE I BETA SUBUNIT.
GN AT2G39550.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
RN NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RX MEDLINE-20083487; PubMed-10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Motil K.S.,
RA Cronin L.A., Shen M., Vanden S.E., Unayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carreira A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhagen G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Lin X.;
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC004218; AAC27846.1; -;
DR HSSP: 002293; IPTI.
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; prenyltrans; 5.
DR Transferase.
SQ SEQUENCE 375 AA; 41472 MW; 4D7919F3F3A695DF CRC64;

Query Match 14.2%; Score 342.5; DB 10; Length 375;
Best Local Similarity 28.18; Pred. No. 7.8e-23;
Matches 110; Conservative 60; Mismatches 117; Indels 105; Gaps 15;

QY 63 ROCHIEYLTQGLRHMGAFVLDANRPWLCYMWV---HPLALDEALDDLENDITFLA 119
Db 37 KDRHLMYLEMVEYLLPYHOSQENIRLTLAHTIISGLHFGARDVCKDVAKWLSFOA 96

```

QY 120 ----RCODKGGYSGGPG-----QLP-----HLATTAAYANFLVTIGSERALSS 159
DB 97 PPTNRYSLKDGFEYGFPGSRSSOPFIENDOLKNGHSLASTCALAIKLYCHD--LST 154
QY 160 INRGALYNLMLOAKVSCAFR-MHDGGEIDVRASYTAISVSLVNI---LDFRLAKGYGD 215
DB 155 IDSKSLISMILQDDDSFMPHIGGETDLRFYCAACAAICVMDMSQMDRESAK---N 211
QY 216 YIARQYEGCIAGEPYAEAHGTYPCGLAAL-----ILLNBAEK--VDLPSTLQIM 264
DB 212 YILNQGSDGCGFGLIPGSESHGANTYCAIASLRLMGTYIGVLLDSNSSSIIDPILLNM 271
QY 265 VAFRCQEGCEGFGRTNKLVDCCYGFMOGAIAITOKLITVDKOLKSSYCKRPSGEDAC 324
DB 272 CLORANDGEGFGRTNKPSPDYCAFWIGAVL---KLI-----GDA- 309
QY 325 STSYGCTAKKSSAVDAKFGPFIOQSNQIGPLFNILAOOYILLCGQVLEGGLRDP 384
DB 310 -----LIDKMLRKFLKMSC-QSKYCGFSKFP 334
QY 385 GANRDHYHSCYCLSGLAVSQYSAMTDTGSCPL 416
DB 335 GOLPDLHSHY-----GYTASLLEBOGLSPL 361

RESULT 10
Q9LHL5 PRELIMINARY: PRT: 317 AA.
AC Q9LHL5:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GERANYLGERANYL TRANSFERASE BETA SUBUNIT (GERANYLGERANYL TRANSFERASE
DE TYPE II BETA SUBUNIT, PUTATIVE).
GN T21B14.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RA Farman M., Lemcke K., Rieger H., Perez-Alonso M., Obermaier B.,
RA Salenoubat M., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA De Simone V., Boutry M., Griwell L.A., Mache R., Pulgadenreich B.,
RA Mincker P., Catolico L., Weissenbach J., Robert C., Brottier P.,
RA Schreier M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Dronek H., Erle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Schaefer M., Schoen O., Barques M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchmann D.,
RA Cooke R., Lande M., Berger-Liandro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,

```

```

RA Monfort A., Argiriou A., Flores M., Ligouri R., Vitale D.,
RA Manhaupt G., Haase D., Schoof H., Ruid S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Malt S., Malt R., Wu D., Peterson J., Van Aken S.,
RA Cressy T.H., Haas B., Malt R., Malt R., Malt R., Malt R., Malt R.,
RA Pail G., Malt R., Malt R., Malt R., Malt R., Malt R., Malt R.,
RA Prens D., Lin X., Nleman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsuno M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana."
RL Nature 408:820-822(2000).
DR EMBL: AP002040; BAB03119.1;
DR EMBL: AP002063; BAB03119.1; JOINED.
DR EMBL: AC069473; AAC01055.1;
DR HSSP: 002293.1P1.
DR InterPro: IPR001330; Prenyltrans.
DR Pfam: PF00432; Prenyltrans; 6.
SQ
SEQUENCE 317 AA: 35192 MW: 02705755FP230843 CRC64;

```

```

Query Match 13.9% Score 336; DB 10: Length 317;
Best Local Similarity 26.4%; Pred. No. 2.4e-22;
Matches 90; Conservative 60; Mismatches 129; Indels 62; Gaps 6;

```

```

QY 83 VLDANRPLCTWVHPALDLDEALDDLENDIIDFLARCQDKGSGGPGQLPHLAVTY 142
DB 30 VMDHLRMNGATYVGLTTLALLDK-LGSVSEDEVSVSWTCHESGCFACNTGHDPHVYTL 88
QY 143 AAVNTLYTIGSERALSSINRNLVFMLOKDVSAFRMIDGGEIDVRASYTAISVSLV 202
DB 89 SAVOILALFDK---LNLIDVEKVSNTYTAGLONEDSGISGDINVENTRSTYIAICSLIL 145
QY 203 NILDFRLAKGYGDYIARQYEGCIAGEPYAEAHGTYPCGLAALILLNBAEKVDLP 262
DB 146 KCLDILNKKAVDYIVSCNLDGFGGSPGAESHAQOIFCCVAGALITGNLRVKKDLG 205
QY 263 GNVAFRCQEGVEG-GFGGRTNKLVDCCYGFMOGAIAITOKLITVDKOLKSSYCKRPSGE 321
DB 206 WMLCERDOYESGGLNGRKLDPDYCSMWVLSLIMIDRY-----LAKFILDSDMDNGGIS 245
QY 322 DKCSSTSYGCTAKKSSAVDAKFGPFIOQSNQIGPLFNILAOOYILLCGQVLEGGLR 381
DB 246 -----HWIEKAR-----LAKFILDSDMDNGGIS 269
QY 382 DKGRNRDHYHSCYCLSGLAVSQYSAM-TDTGSCPLPOHYL 421
DB 270 DRPSTYVDIPIHYGVAGLSLELPEVGVKTIDPAVALPVHVI 310

RESULT 11
Q9PPP6 PRELIMINARY: PRT: 376 AA.
AC Q9PPP6:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GERANYLGERANYL TRANSFERASE BETA SUBUNIT.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN 11
RP SEQUENCE FROM N.A.
RC MEDLINE=21392285; Pubmed=11500541;
RA Caldelari D., Sternberg H., Rodriguez-Concepcion M., Grusissem W.,
RA Valovsky S.;
RT "Efficient prenylation by a plant geranylgeranyltransferase-I requires
a functional Caab box motif and a proximal polybasic domain."

```


Plant Physiol. 126:1416-1429(2001).
RL EMBL: AF311225; AAC40865.1; -
DR HSSP: 002293; 1FT1.
DR InterPro: IPR001330; Premyltrans.
DR Pfam: PF00432; premyltrans; 5.
DR Transferase.
SQ SEQUENCE 376 AA; 41967 MW; 753A7B74210EFD1B CRC64;
Query Match 13.4%; Score 322.5; DB 10; Length 376;
Best Local Similarity 27.0%; Pred. No. 5,3e-21;
Matches 109; Conservative 57; Mismatches 108; Indels 129; Gaps 17;
OY 57 IMLEL-----MNDQHIEVLT-----POLRHMGP-----AFHVLDANK----- 88
DB 46 MMYELLPRHYQSQEIINRTLAHFTTSLGHLFGKARDVRYVAKWVLSQAFPTARVSLK 105
OY 89 PWLCYMWVHPLALDEALDDLENDIIDFLARCOCDKDGSGGPGQULPLATTYAANTL 148
DB 106 RMRILMFWKGVLSFPL-----MKNDGLHNKS-----HLASTYCALAIL 146
OY 149 VTIGSERLSSINGNLYNFMLOKNDVSAFR-MHDSGEIDVRASTYASVSLVNT--- 204
DB 147 KYIGHD--LSTIDSKSLISMTINQQDGSFMPHIGGEDLFYVCAALICYMLDSWG 204
OY 205 LDFKLAKGVGDYIARCOYTEGGIAGPEPYAEAHGVTFCGLAAL-----ILINAEK 255
DB 205 MDKESAK---NYILNCSYDDGFCFLIGSESHGATYCAIASRLMGVIGVLLDNDSS 261
OY 256 --VDLPISLIGVAVRQGVGEGFQGTNRKLVYDGCYSFMOCAGALFTOKLTYYDKOLKSSY 313
DB 262 STIDPSLLNCLDQKANDGFGQRTKPSDCTAFMIGAVL---KLL--- 306
OY 314 SCKRPSGSDACSTSSYCGTAKKSSAVDVAKFGFDFLQOSNOIGPLFNHIALQOYILCS 373
DB 307 -----GGDA-----LIDRMALRKFLMSC- 324
OY 374 GYLEGGLDRPKNRNDHYHSCYCLSGLAIVSAMSMDTGSCLP 416
DB 325 GSKYCGFSKFPQGLPDLHYHSTY-----GYTAFSLLEBOGSSPL 362
RESULT 12
OYXZ68
ID OYXZ68 PRELIMINARY; PRT: 347 AA.
RC STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Ramatatidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Bratton R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abrill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howard T.J., Wei M.-H., Ibegwan C.,
Jalali M., Kalusi F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
Palazzo M., Piatton G.S., Pan S., Polard J., Pui V., Reese M.G.,
Reichert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spindling A.C., Stapleton M., Strong R., Sun E.,
Svitskas R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CANTON S;
RA Avedisov S.N., Thomas B.J.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Y, CN BW SP;
RA Stapleton M., Brickstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarini H., Li P., Liao G., Miranda A.L., Mungall C.J.,
R. Nuno J., Paclet J., Paragas V., Park S., Phouanavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celinker S.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003581; AAES1183.1; -
DR EMBL: AF133269; AAD33042.1; -
DR EMBL: AY060784; AAL28332.1; -
DR HSSP: 002293; 1FT1.
DR Flybase: FBgn0028970; beta-ggt-II.
DR InterPro: IPR001330; Premyltrans.
DR Pfam: PF00432; premyltrans; 5.
KW Transferase.
SQ SEQUENCE 347 AA; 38542 MW; 7BF74887548E1B4 CRC64;
Query Match 12.6%; Score 304.5; DB 5; Length 347;
Best Local Similarity 23.6%; Pred. No. 2,1e-19;
Matches 90; Conservative 62; Mismatches 136; Indels 93; Gaps 9;
OY 59 LEIMRDQHIEVLT-----LTPGLRHMGPAPHVLDANKRPLCYMWVHPLALDE 104
DB 29 LQFWK--HVEYLEHNKQEDDY EYCMTEFLMSG-----ITWGTTALDIMGQ 73
OY 105 ALDDLENDIIDFLARCO-DRKDGYSGGPGOLPLATTYAANTLVTIGSESRALSINSG 163
DB 74 -LEIRERSIIIEFVARKCCPMTGFGFACCEGHDPILYTTLSAIGILTVD--ALEIDRE 129
OY 164 NLXNFMLOKNDVSAFRMNDGGEIDVRASTYASVSLVILD--FKLAKGVGDYIARCO 221
DB 130 AVAFRVAAGIQDPDGSFFQDKWGEVDTRSRCAVASLTLGLRMQTTIDVKAKEFVLSGN 189
OY 222 TTEGGIAGEPYAEAGVTFCGLAALLILNEAEVNDPISLIGVAVRQGVGEGFQGTNRK 281
DB 190 QTDGCGSGSPAESNAGLITCYCGVFSLTRHLDVDKRGMLCERQPLSGUNGRLPEK 249
OY 282 LVDGCSFPMOCAGALFTOKLTYYDKOLKSSYSCRRPSGSDACSTSYCGTAKKSSAVD 341
DB 250 LDDVCSMWVVASLITMGRHLWISSEK----- 276
OY 342 YAKFGDFLQOSNOIGPLFNHIALQOYILCSGYLEGGLDRPKNRNDHYHSCYCLSGLA 401


```

Matches 101; Conservative 55; Mismatches 122, Indels 110; Gaps 14
QY 85 DANKPWLCTVYMHAPLALD--EALDDLENDIIIFL-----ARCQDKD--GYISGGRGDI 135
Db 34 DNRSTVEFAVCGDLVNSLHVPPOLRDIDIMIVYGLVPPDRDNKRCNCGMGCCRAV 93
QY 136 P-----HATTYAAVNTLVLTIGSERALSSINGNLNYEMLMKDYSGA 178
Db 94 PKEDAEIIECHRNMYMGHLANTYISLAVLTIGDD--LSHLDKRSIYDGVAAVQKPEGS 151
QY 179 F-RMHDCGETDVASYTAISVASLVNIILDFKIAKGVGDYIARCTQYEGGIAGEPYAEAHG 237
Db 152 FSACIDGSEDDMFVYCAATTCYMLDYMOWDKVETMFQIFRSLRYDYGFSGOIELEGANG 211
QY 238 GYFFCGALAILLINEAEKVD---LESLSIGVAFFRGVCGCGGRTKLVLCGCSIFWGAA 294
Db 212 GTFFCALAAHLHSGOHRIRDAITVYRMRKMLIFRQ--MDGFQGRPNRPVDTCSFWFGAS 269
QY 295 IAFQKLITIVDKQLKSSYSCKRRPGEDACSTSYGCTAKKSSAVYAKAFGEFDIGQSN 354
Db 270 L-----CLIDGSELT-----DYAR----- 283
QY 355 QIGPFLHNIALQOYIILCSQVLEGGILRDKPCKNRRDHVHSCYCLISGLAVSQYSAMTDTGSC 414
Db 284 -----NREFIILSTODKILIGFAFWKPOATPDPFRHYIIGLIGLAF-----TGE- 324
QY 415 PLPOHVLGPRYNLLEPIHPLVNVLDKY 442
Db 325 --PG-----LSPVNPISLMSMAAY 341

```

RESULT	15
ID	018197
AC	018197; PRELIMINARY;
DT	01-JAN-1998 (TrEMBLrel_05, Created)
DR	01-MAY-1999 (TrEMBLrel_10, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel_19, Last annotation update)
DE	Y48ELB.3 PROTEIN.
GN	Y48ELB.3.
OS	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
CC	Rhabdilitidae; Peleiderinae; Caenorhabditis.
OX	NCBI_TaxID=6239;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	McKurray A. A.;
RL	Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=99069613; PubMed=9851916;
RA	none;
RT	"genome sequence of the nematode C.elegans: A platform for
RV	investigating biology.";
RL	Science 282:2012-2018(1998).
EMBL	Z93393; CAB07699.1;"
DR	InterPro: IPR001330; Pfam: Pflam.Pf00432; Pfam: Pf00432; Pfam: Pf00432; Pfam: Pf00432;
DR	Pfam: Pf00432; Pfam: Pf00432; Pfam: Pf00432; Pfam: Pf00432;
SO	SEQUENCE 360 AA; 40351 MW; C8C7E69CE8716969 CRC64;

Query Match	10.1%;	Score 244.5;	DB 5;	Length 360;
Best Local Similarity	22.8%;	Pred. No. 6.9e-14;		
Matches 91;	Conservative 70;	Mismatches 128;	Indels 111;	Gaps 16;

```

Oy 65 QHTEYLPGLRHMGAFAHFLNARPMYLCYMMVHEFLA---LEPALDDLENDIIDFLARC 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 31 KHIGELIRHLNFWPQRYMTELSRNTIFLEAISLDLCELDMLLPERRQCAIDWITGL 90
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 122 ODDGGVSGSPG-----QLPHLTAAVNTLVLTGSEPAALSIIRGLYNYEFLQM 172
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 91 QPFGNVCVCGFRSHSCENSIDEAFLKQTTLSALSLAIGDD--LKKDRAKAIKTYKTA 148
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 173 KDVSQGFRRMHD--GGEIDVRASTAYTASVASLVN-----ILDF--KLAKGVGDYIARCQTYEG 225

```

Db	149	GRNGCFMNGSGVSESDMRREFCAVAISHIIDDKDCKDTIMWKLA-----GFLRSLNIDG	204
Qy	226	GIAGEPYAARHGCGYTFPGSLAAILLNE--AEKV-----DLPSLIGNVAARQGVCEGFGORT	279
Db	205	GICDAFGDESHGGSTFCALIASLALSNLRMTVEEVLTRRDDRLIRMAIQKODI--GFGIRA	262
Qy	280	NKLVDGCSYFMOGAAIAFTOKLITITVDKQLSSYCKRPDGEDACSTSSYCGTAKKSSSA	339
Db	263	HKYDDSCYAFMWIGA-----TLKIL-----NAYHLYSKOH---	291
Qy	340	VDYAKFGDFEIOQSNIDGPLEFNIALAQVILLCSQVLEGL--RDKPGRNDRHSCYL	397
Db	292	-----LRPELMIGQNHPIGCFCKYPERGQYSDLIHLYFSI	328
Qy	398	SGLAVQYSAMTDTGSCPLRQHVILGAPYSNILEPNIHYLVYV	437
Db	327	AAIS-----LLG--EPRAVNVHPSLVN	346

Search completed: November 1, 2002, 18:09:14
Job time : 69 secs

THIS PAGE BLANK (USPTO)